

SEQUENCE LISTING

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- (1) GENERAL INFORMATION:
- (i) APPLICANT: MIYAZONO, Kohei
TEN DIJKE, Peter
FRANZEN, Petra
YAMASHITA, Hidetoshi
HELDIN, Carl-Henrik
- (ii) TITLE OF INVENTION: ACTIVIN RECEPTOR LIKE KINASES, PROTEINS
HAVING SERINE THREONINE KINASE DOMAINS,
AND THEIR USE
- (iii) NUMBER OF SEQUENCES: 48
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Fulbright & Jaworski L.L.P.
(B) STREET: 666 Fifth Avenue
(C) CITY: New York City
(D) STATE: New York
(E) COUNTRY: USA
(F) ZIP: 10103
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
(B) COMPUTER: IBM PS/2
(C) OPERATING SYSTEM: PC-DOS
(D) SOFTWARE: Wordperfect
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: 09/903,068
(B) FILING DATE: July 11, 2001
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/436,265
(B) FILING DATE: October 30, 1995
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: PCT/GB93/02367
(B) FILING DATE: November 17, 1993
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: GB 9224057.1
(B) FILING DATE: November 17, 1992
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: GB 9304677.9
(B) FILING DATE: March 8, 1993
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: GB 9304680.3
(B) FILING DATE: March 8, 1993
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 9311047.6
(B) FILING DATE: May 28, 1993

- (vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: 9313763.6
 (B) FILING DATE: July 2, 1993
- (vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: 9316099.2
 (B) FILING DATE: August 3, 1993
- (vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: 321344.5
 (B) FILING DATE: October 15, 1993
- (viii) ATTORNEY/AGENT INFORMATION:
 (A) NAME: Norman D. Hanson
 (B) REGISTRATION NUMBER: 30,946
 (C) REFERENCE/DOCKET NUMBER: LUD 5298.4 DIV (10105901)
- (ix) TELECOMMUNICATION INFORMATION:
 (A) TELEPHONE: (212) 318-3000
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(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1984 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 283..1791
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
- | | |
|---|-----|
| AGGAAACGGT TTATTAGGAG GGAGTGGTGG AGCTGGGCCA GGCAGGAAGA CGCTGGAATA | 60 |
| AGAAACATTT TTGCTCCAGC CCCATCCCA GTCCCGGGAG GCTGCCGCGC CAGCTGCGCC | 120 |
| GAGCGAGCCC CTCGCCGGCT CCAGCCCGGT CCGGGGCCGC GCCGGACCCC AGCCCGCCGT | 180 |
| CCAGCGCTGG CGGTGCAACT GCGGCCGCGC GGTGGAGGGG AGGTGGCCCC GTCCGCCGA | 240 |
| AGGCTAGCGC CCCGCCACCC GCAGAGCGGG CCCAGAGGGA CC ATG ACC TTG GGC | 294 |
| Met Thr Leu Gly | |
| 1 | |
| TCC CCC AGG AAA GGC CTT CTG ATG CTG CTG ATG GCC TTG GTG ACC CAG | 342 |
| Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala Leu Val Thr Gln | |
| 5 10 15 20 | |
| GGA GAC CCT GTG AAG CCG TCT CGG GGC CCG CTG GTG ACC TGC ACG TGT | 390 |
| Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val Thr Cys Thr Cys | |
| 25 30 35 | |
| GAG AGC CCA CAT TGC AAG GGG CCT ACC TGC CGG GGG GCC TGG TGC ACA | 438 |
| Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly Ala Trp Cys Thr | |
| 40 45 50 | |
| GTA GTG CTG GTG CGG GAG GAG GGG AGG CAC CCC CAG GAA CAT CGG GGC | 486 |
| Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln Glu His Arg Gly | |
| 55 60 65 | |

TGC GGG AAC TTG CAC AGG GAG CTC TGC AGG GGG CGC CCC ACC GAG TTC	534
Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg Pro Thr Glu Phe	
70 75 80	
GTC AAC CAC TAC TGC TGC GAC AGC CAC CTC TGC AAC CAC AAC GTG TCC	582
Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn His Asn Val Ser	
85 90 95 100	
CTG GTG CTG GAG GCC ACC CAA CCT CCT TCG GAG CAG CCG GGA ACA GAT	630
Leu Val Leu Glu Ala Thr Gln Pro Pro Glu Gln Pro Gly Thr Asp	
105 110 115	
GGC CAG CTG GCC CTG ATC CTG GGC CCC GTG CTG GCC TTG CTG GCC CTG	678
Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala Leu Leu Ala Leu	
120 125 130	
GTG GCC CTG GGT GTC CTG GGC CTG TGG CAT GTC CGA CGG AGG CAG GAG	726
Val Ala Glu Gly Val Leu Gly Leu Trp His Val Arg Arg Arg Gln Glu	
135 140 145	
AAG CAG CGT GGC CTG CAC AGC GAG CTG GGA GAG TCC AGT CTC ATC CTG	774
Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser Ser Leu Ile Leu	
150 155 160	
AAA GCA TCT GAG CAG GGC GAC ACG ATG TTG GGG GAC CTC CTG GAC AGT	822
Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp Leu Leu Asp Ser	
165 170 175 180	
GAC TGC ACC ACA GGG AGT GGC TCA GGG CTC CCC TTC CTG GTG CAG AGG	870
Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe Leu Val Gln Arg	
185 190 195	
ACA GTG GCA CGG CAG GTT GCC TTG GTG GAG TGT GTG GGA AAA GGC CGC	918
Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val Gly Lys Gly Arg	
200 205 210	
TAT GGC GAA GTG TGG CGG GGC TTG TGG CAC GGT GAG AGT GTG GCC GTC	966
Tyr Gly Glu Val Trp Arg Gly Leu Trp His Gly Glu Ser Val Ala Val	
215 220 225	
AAG ATC TTC TCC TCG AGG GAT GAA CAG TCC TGG TTC CGG GAG ACT GAG	1014
Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe Arg Glu Thr Glu	
230 235 240	
ATC TAT AAC ACA GTA TTG CTC AGA CAC GAC AAC ATC CTA GGC TTC ATC	1062
Ile Tyr Asn Thr Val Leu Arg His Asp Asn Ile Leu Gly Phe Ile	
245 250 255 260	
GCC TCA GAC ATG ACC TCC CGC AAC TCG AGC ACG CAG CTG TGG CTC ATC	1110
Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln Leu Trp Leu Ile	
265 270 275	
ACG CAC TAC CAC GAG CAC GGC TCC CTC TAC GAC TTT CTG CAG AGA CAG	1158
Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe Leu Gln Arg Gln	
280 285 290	
ACG CTG GAG CCC CAT CTG GCT CTG AGG CTA GCT GTG TCC GCG GCA TGC	1206
Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val Ser Ala Ala Cys	
295 300 305	
GGC CTG GCG CAC CTG CAC GTG GAG ATC TTC GGT ACA CAG GGC AAA CCA	1254
Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr Gln Gly Lys Pro	
310 315 320	
GCC ATT GCC CAC CGC GAC TTC AAG AGC CGC AAT GTG CTG GTC AAG AGC	1302
Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val Leu Val Lys Ser	
325 330 335 340	
AAC CTG CAG TGT TGC ATC GCC GAC CTG GGC CTG GCT GTG ATG CAC TCA	1350
Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala Val Met His Ser	
345 350 355	
CAG GGC AGC GAT TAC CTG GAC ATC GGC AAC AAC CCG AGA GTG GGC ACC	1398
Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro Arg Val Gly Thr	
360 365 370	

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AAG CGG TAC ATG GCA CCC GAG GTG CTG GAC GAG CAG ATC CGC ACG GAC      1446
Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln Ile Arg Thr Asp
375                               380                               385
TGC TTT GAG TCC TAC AAG TGG ACT GAC ATC TGG GCC TTT GGC CTG GTG      1494
Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala Phe Gly Leu Val
390                               395                               400
CTG TGG GAG ATT GCC CGC CGG ACC ATC GTG AAT GGC ATC GTG GAG GAC      1542
Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly Ile Val Glu Asp
405                               410                               415                               420
TAT AGA CCA CCC TTC TAT GAT GTG GTG CCC AAT GAC CCC AGC TTT GAG      1590
Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp Pro Ser Phe Glu
425                               430                               435
GAC ATG AAG AAG GTG GTG TGT GTG GAT CAG CAG ACC CCC ACC ATC CCT      1638
Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro Thr Ile Pro
440                               445                               450
AAC CGG CTG GCT GCA GAC CCG GTC CTC TCA GGC CTA GCT CAG ATG ATG      1686
Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala Gln Met Met
455                               460                               465
CGG GAG TGC TGG TAC CCA AAC CCC TCT GCC CGA CTC ACC GCG CTG CGG      1734
Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg
470                               475                               480
ATC AAG AAG ACA CTA CAA AAA ATT AGC AAC AGT CCA GAG AAG CCT AAA      1782
Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro Glu Lys Pro Lys
485                               490                               495                               500
GTG ATT CAA TAGCCCAGGA GCACCTGATT CCTTCTGCC TGCAGGGGGC      1831
Val Ile Gln

TGGGGGGGTG GGGGGCAGTG GATGGTGCCC TATCTGGGTA GAGGTAGTGT GAGTGTGGTG      1891
TGTGCTGGGG ATGGGCAGCT GCGCCTGCCT GCTCGGCCCC CAGCCACCCC AGCCAAAAAT      1951
ACAGCTGGGC TGAAACCTGA AAAAAAAAAA AAA      1984

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(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 503 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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Met Thr Leu Gly Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala
1           5           10           15
Leu Val Thr Gln Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val
20           25           30
Thr Cys Thr Cys Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly
35           40           45
Ala Trp Cys Thr Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln
50           55           60
Glu His Arg Gly Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg
65           70           75           80
Pro Thr Glu Phe Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn
85           90           95
His Asn Val Ser Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln
100          105          110
Pro Gly Thr Asp Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala
115          120          125
Leu Leu Ala Leu Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg
130          135          140

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Arg Arg Gln Glu Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser
145          150          155          160
Ser Leu Ile Leu Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp
          165          170          175
Leu Leu Asp Ser Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe
          180          185          190
Leu Val Gln Arg Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val
          195          200          205
Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Leu Trp His Gly Glu
          210          215          220
Ser Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe
225          230          235          240
Arg Glu Thr Glu Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile
          245          250          255
Leu Gly Phe Ile Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln
          260          265          270
Leu Trp Leu Ile Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe
          275          280          285
Leu Gln Arg Gln Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val
          290          295          300
Ser Ala Ala Cys Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr
305          310          315          320
Gln Gly Lys Pro Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val
          325          330          335
Leu Val Lys Ser Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala
          340          345          350
Val Met His Ser Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro
          355          360          365
Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln
          370          375          380
Ile Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala
385          390          395          400
Phe Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly
          405          410          415
Ile Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp
          420          425          430
Pro Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr
          435          440          445
Pro Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu
          450          455          460
Ala Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu
465          470          475          480
Thr Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro
          485          490          495
Glu Lys Pro Lys Val Ile Gln
          500

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(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2724 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 104..1630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CTCCGAGTAC CCCAGTGACC AGAGTGAGAG AAGCTCTGAA CGAGGGCACG CGGCTTGAAG 60
 GACTGTGGGC AGATGTGACC AAGAGCCTGC ATTAAGTTGT ACA ATG GTA GAT GGA 115
 Met Val Asp Gly
 1
 GTG ATG ATT CTT CCT GTG CTT ATC ATG ATT GCT CTC CCC TCC CCT AGT 163
 Val Met Ile Leu Pro Val Leu Ile Met Ile Ala Leu Pro Ser Pro Ser
 5 10 15 20
 ATG GAA GAT GAG AAG CCC AAG GTC AAC CCC AAA CTC TAC ATG TGT GTG 211
 Met Glu Asp Glu Lys Pro Lys Val Asn Pro Lys Leu Tyr Met Cys Val
 25 30 35
 TGT GAA GGT CTC TCC TGC GGT AAT GAG GAC CAC TGT GAA GGC CAG CAG 259
 Cys Glu Gly Leu Ser Cys Gly Asn Glu Asp His Cys Glu Gly Gln Gln
 40 45 50
 TGC TTT TCC TCA CTG AGC ATC AAC GAT GGC TTC CAC GTC TAC CAG AAA 307
 Cys Phe Ser Ser Leu Ser Ile Asn Asp Gly Phe His Val Tyr Gln Lys
 55 60 65
 GGC TGC TTC CAG GTT TAT GAG CAG GGA AAG ATG ACC TGT AAG ACC CCG 355
 Gly Cys Phe Gln Val Tyr Glu Gln Gly Lys Met Thr Cys Lys Thr Pro
 70 75 80
 CCG TCC CCT GGC CAA GCT GTG GAG TGC TGC CAA GGG GAC TGG TGT AAC 403
 Pro Ser Pro Gly Gln Ala Val Glu Cys Cys Gln Gly Asp Trp Cys Asn
 85 90 95 100
 AGG AAC ATC ACG GCC CAG CTG CCC ACT AAA GGA AAA TCC TTC CCT GGA 451
 Arg Asn Ile Thr Ala Gln Leu Pro Thr Lys Gly Lys Ser Phe Pro Gly
 105 110 115
 ACA CAG AAT TTC CAC TTG GAG GTT GGC CTC ATT ATT CTC TCT GTA GTG 499
 Thr Gln Asn Phe His Leu Glu Val Gly Leu Ile Ile Leu Ser Val Val
 120 125 130
 TTC GCA GTA TGT CTT TTA GCC TGC CTG CTG GGA GTT GCT CTC CGA AAA 547
 Phe Ala Val Cys Leu Leu Ala Cys Leu Leu Gly Val Ala Leu Arg Lys
 135 140 145
 TTT AAA AGG CGC AAC CAA GAA CGC CTC AAT CCC CGA GAC GTG GAG TAT 595
 Phe Lys Arg Arg Asn Gln Glu Arg Leu Asn Pro Arg Asp Val Glu Tyr
 150 155 160
 GGC ACT ATC GAA GGG CTC ATC ACC ACC AAT GTT GGA GAC AGC ACT TTA 643
 Gly Thr Ile Glu Gly Leu Ile Thr Thr Asn Val Gly Asp Ser Thr Leu
 165 170 175 180
 GCA GAT TTA TTG GAT CAT TCG TGT ACA TCA GGA AGT GGC TCT GGT CTT 691
 Ala Asp Leu Leu Asp His Ser Cys Thr Ser Gly Ser Gly Ser Gly Leu
 185 190 195
 CCT TTT CTG GTA CAA AGA ACA GTG GCT CGC CAG ATT ACA CTG TTG GAG 739
 Pro Phe Leu Val Gln Arg Thr Val Ala Arg Gln Ile Thr Leu Leu Glu
 200 205 210
 TGT GTC GGG AAA GGC AGG TAT GGT GAG GTG TGG AGG GGC AGC TGG CAA 787
 Cys Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Ser Trp Gln
 215 220 225
 GGG GAA AAT GTT GCC GTG AAG ATC TTC TCC TCC CGT GAT GAG AAG TCA 835
 Gly Glu Asn Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Lys Ser
 230 235 240
 TGG TTC AGG GAA ACG GAA TTG TAC AAC ACT GTG ATG CTG AGG CAT GAA 883
 Trp Phe Arg Glu Thr Glu Leu Tyr Asn Thr Val Met Leu Arg His Glu

245	250	255	260	
AAT ATC TTA GGT TTC	ATT GCT TCA GAC ATG	ACA TCA AGA CAC	TCC AGT	931
Asn Ile Leu Gly Phe	Ile Ala Ser Asp Met	Thr Ser Arg His	Ser Ser	
265	270	275		
ACC CAG CTG TGG TTA	ATT ACA CAT TAT CAT	GAA ATG GGA TCG	TTG TAC	979
Thr Gln Leu Trp Leu	Ile Thr His Tyr His	Glu Met Gly Ser	Leu Tyr	
280	285	290		
GAC TAT CTT CAG CTT	ACT ACT CTG GAT	ACA GTT AGC TGC	CTT CGA	1027
Asp Tyr Leu Gln Leu	Thr Thr Leu Asp	Thr Val Ser Cys	Leu Arg	
295	300	305		
GTG CTG TCC ATA GCT	AGT GGT CTT GCA	CAT TTG CAC	ATA GAG	1075
Val Leu Ser Ile Ala	Ser Gly Leu Ala	His Leu His	Ile Glu	
310	315	320		
GGG ACC CAA GGG AAA	CCA GCC ATT GCC	CAT CGA GAT	TTA AAG	1123
Gly Thr Gln Gly Lys	Pro Ala Ile Ala	His Arg Asp	Leu Lys	
325	330	335	340	
AAT ATT CTG GTT AAG	AAG AAT GGA CAG	TGT TGC ATA	GCA GAT	1171
Asn Ile Leu Val Lys	Lys Asn Gly Gln	Cys Cys Ile	Ala Asp	
345	350	355		
CTG GCA GTC ATG CAT	TCC CAG AGC ACC	AAT CAG CTT	GAT GTG	1219
Leu Ala Val Met His	Ser Gln Ser Thr	Asn Gln Leu	Asp Val	
360	365	370		
AAT CCC CGT GTG GGC	ACC AAG CGC TAC	ATG GCC CCC	GAA GTT	1267
Asn Pro Arg Val Gly	Thr Lys Arg Tyr	Met Ala Pro	Glu Val	
375	380	385		
GAA ACC ATC CAG GTG	GAT TGT TTC GAT	TCT TAT AAA	AGG GTC	1315
Glu Thr Ile Gln Val	Asp Cys Phe Asp	Ser Tyr Lys	Arg Val	
390	395	400		
TGG GCC TTT GGA CTT	GTT TTG TGG GAA	GTG GCC AGG	CGG ATG	1363
Trp Ala Phe Gly Leu	Val Leu Trp Glu	Val Ala Arg	Arg Met	
405	410	415	420	
AAT GGT ATA GTG GAG	GAT TAC AAG CCA	CCG TTC TAC	GAT GTG	1411
Asn Gly Ile Val Glu	Asp Tyr Lys Pro	Pro Phe Tyr	Asp Val	
425	430	435		
AAT GAC CCA AGT TTT	GAA GAT ATG AGG	AAG GTA GTC	TGT GTG	1459
Asn Asp Pro Ser Phe	Glu Asp Met Arg	Lys Val Val	Cys Val	
440	445	450		
CAA AGG CCA AAC ATA	CCC AAC AGA TGG	TTC TCA GAC	CCG ACA	1507
Gln Arg Pro Asn Ile	Pro Asn Arg Trp	Phe Ser Asp	Pro Thr	
455	460	465		
TCT CTG GCC AAG CTA	ATG AAA GAA TGC	TGG TAT CAA	AAT CCA	1555
Ser Leu Ala Lys Leu	Met Lys Glu Cys	Trp Tyr Gln	Asn Pro	
470	475	480		
AGA CTC ACA GCA CTG	CGT ATC AAA AAG	ACT TTG ACC	AAA ATT	1603
Arg Leu Thr Ala Leu	Arg Ile Lys Lys	Thr Leu Thr	Lys Ile	
485	490	495	500	
TCC CTC GAC AAA TTG	AAA ACT GAC TGT	TGACATTTTC	ATAGTGTC	1650
Ser Leu Asp Lys Lys	Thr Asp Cys			
505				
GAAGGAAGAT TTGACGTTGT	TGTCATTGTC CAGCTGGGAC	CTAATGCTGG CCTGACTGGT		1710
TGTCAGAATG GAATCCATCT	GTCTCCCTCC CCAAATGGCT	GCTTTGACAA GGCAGACGTC		1770
GTACCCAGCC ATGTGTTGGG	GAGACATCAA AACCACTCTA	ACCTCGCTCG ATGACTGTGA		1830
ACTGGGCATT TCACGAACCTG	TTCACACTGC AGAGACTAAT	GTTGGACAGA CACTGTTGCA		1890
AAGGTAGGGA CTGGAGGAAC	ACAGAGAAAT CCTAAAAGAG	ATCTGGGCAT TAAGTCAGTG		1950
GCTTTGCATA GCTTTCACAA	GTCTCCTAGA CACTCCCCAC	GGGAACTCA AGGAGGTGGT		2010
GAATTTTAA TCAGCAATAT	TGCCTGTGCT TCCTCTTTT	ATTGCACTAG GAATTCTTTG		2070
CATTCCTTAC TTGCACTGTT	ACTCTTAATT TTAAAGACCC	AACTTGCCAA AATGTTGGCT		2130

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GCGTACTCCA CTGGTCTGTC TTTGGATAAT AGGAATTCAA TTTGGCAAAA CAAAATGTAA 2190
TGTCAGACTT TGTCGCATTT TACACATGTG CTGATGTTTA CAATGATGCC GAACATTAGG 2250
AATTGTTTAT ACACAACTTT GCAAATTATT TATTACTTGT GCACTTAGTA GTTTTACAA 2310
AACTGCTTTG TGCATATGTT AAAGCTTATT TTTATGTGGT CTTATGATTT TATTACAGAA 2370
ATGTTTTTAA CACTATACTC TAAAATGGAC ATTTTCTTTT ATTATCAGTT AAAATCACAT 2430
TTTAAGTGCT TCACATTTGT ATGTGTGTAG ACTGTAACTT TTTTTCAGTT CATATGCAGA 2490
ACGTATTTAG CCATTACCCA CGTGACACCA CCGAATATAT TATCGATTTA GAAGCAAAGA 2550
TTTCAGTAGA ATTTTAGTCC TGAACGCTAC GGGGAAAATG CATTTTCTTC AGAATTATCC 2610
ATTACGTGCA TTAAACTCT GCCAGAAAAA AATAACTATT TTGTTTTAAT CTACTTTTTC 2670
TATTTAGTAG TTATTTGTAT AAATTAAATA AACTGTTTTT AAGTCAAAAA AAAA 2724

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(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 509 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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Met Val Asp Gly Val Met Ile Leu Pro Val Leu Ile Met Ile Ala Leu
1      5      10      15
Pro Ser Pro Ser Met Glu Asp Glu Lys Pro Lys Val Asn Pro Lys Leu
20     25     30
Tyr Met Cys Val Cys Glu Gly Leu Ser Cys Gly Asn Glu Asp His Cys
35     40     45
Glu Gly Gln Gln Cys Phe Ser Ser Leu Ser Ile Asn Asp Gly Phe His
50     55     60
Val Tyr Gln Lys Gly Cys Phe Gln Val Tyr Glu Gln Gly Lys Met Thr
65     70     75     80
Cys Lys Thr Pro Pro Ser Pro Gly Gln Ala Val Glu Cys Cys Gln Gly
85     90     95
Asp Trp Cys Asn Arg Asn Ile Thr Ala Gln Leu Pro Thr Lys Gly Lys
100    105    110
Ser Phe Pro Gly Thr Gln Asn Phe His Leu Glu Val Gly Leu Ile Ile
115    120    125
Leu Ser Val Val Phe Ala Val Cys Leu Leu Ala Cys Leu Leu Gly Val
130    135    140
Ala Leu Arg Lys Phe Lys Arg Arg Asn Gln Glu Arg Leu Asn Pro Arg
145    150    155    160
Asp Val Glu Tyr Gly Thr Ile Glu Gly Leu Ile Thr Thr Asn Val Gly
165    170    175
Asp Ser Thr Leu Ala Asp Leu Leu Asp His Ser Cys Thr Ser Gly Ser
180    185    190
Gly Ser Gly Leu Pro Phe Leu Val Gln Arg Thr Val Ala Arg Gln Ile
195    200    205
Thr Leu Leu Glu Cys Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg
210    215    220
Gly Ser Trp Gln Gly Glu Asn Val Ala Val Lys Ile Phe Ser Ser Arg
225    230    235    240
Asp Glu Lys Ser Trp Phe Arg Glu Thr Glu Leu Tyr Asn Thr Val Met
245    250    255
Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ser Asp Met Thr Ser
260    265    270
Arg His Ser Ser Thr Gln Leu Trp Leu Ile Thr His Tyr His Glu Met
275    280    285
Gly Ser Leu Tyr Asp Tyr Leu Gln Leu Thr Thr Leu Asp Thr Val Ser
290    295    300

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Cys Leu Arg Ile Val Leu Ser Ile Ala Ser Gly Leu Ala His Leu His
 305 310 315 320
 Ile Glu Ile Phe Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp
 325 330 335
 Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Gln Cys Cys Ile
 340 345 350
 Ala Asp Leu Gly Leu Ala Val Met His Ser Gln Ser Thr Asn Gln Leu
 355 360 365
 Asp Val Gly Asn Asn Pro Arg Val Gly Thr Lys Arg Tyr Met Ala Pro
 370 375 380
 Glu Val Leu Asp Glu Thr Ile Gln Val Asp Cys Phe Asp Ser Tyr Lys
 385 390 395 400
 Arg Val Asp Ile Trp Ala Phe Gly Leu Val Leu Trp Glu Val Ala Arg
 405 410 415
 Arg Met Val Ser Asn Gly Ile Val Glu Asp Tyr Lys Pro Pro Phe Tyr
 420 425 430
 Asp Val Val Pro Asn Asp Pro Ser Phe Glu Asp Met Arg Lys Val Val
 435 440 445
 Cys Val Asp Gln Gln Arg Pro Asn Ile Pro Asn Arg Trp Phe Ser Asp
 450 455 460
 Pro Thr Leu Thr Ser Leu Ala Lys Leu Met Lys Glu Cys Trp Tyr Gln
 465 470 475 480
 Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Thr
 485 490 495
 Lys Ile Asp Asn Ser Leu Asp Lys Leu Lys Thr Asp Cys
 500 505

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2932 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 310..1905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GCTCCGCGCC GAGGGCTGGA GGATGCGTTC CCTGGGGTCC GGACTTATGA AAATATGCAT 60
 CAGTTTAATA CTGTCTTGGA ATTCATGAGA TGGAAGCATA GGTCAAAGCT GTTTGGAGAA 120
 AATCAGAAGT ACAGTTTAT CTAGCCACAT CTTGGAGGAG TCGTAAGAAA GCAGTGGGAG 180
 TTGAAGTCAT TGTCAAGTGC TTGCGATCTT TTACAAGAAA ATCTCACTGA ATGATAGTCA 240
 TTTAAATTGG TGAAGTAGCA AGACCAATTA TTAAAGGTGA CAGTACACAG GAAACATTAC 300
 AATTGAACA ATG ACT CAG CTA TAC ATT TAC ATC AGA TTA TTG GGA GCC 348
 Met Thr Gln Leu Tyr Ile Tyr Ile Arg Leu Leu Gly Ala
 1 5 10
 TAT TTG TTC ATC ATT TCT CGT GTT CAA GGA CAG AAT CTG GAT AGT ATG 396
 Tyr Leu Phe Ile Ile Ser Arg Val Gln Gly Gln Asn Leu Asp Ser Met
 15 20 25
 CTT CAT GGC ACT GGG ATG AAA TCA GAC TCC GAC CAG AAA AAG TCA GAA 444
 Leu His Gly Thr Gly Met Lys Ser Asp Ser Asp Gln Lys Lys Ser Glu

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30          35          40          45
AAT GGA GTA ACC TTA GCA CCA GAG GAT ACC TTG CCT TTT TTA AAG TGC      492
Asn Gly Val Thr Leu Ala Pro Glu Asp Thr Leu Pro Phe Leu Lys Cys
50          55          60
TAT TGC TCA GGG CAC TGT CCA GAT GAT GCT ATT AAT AAC ACA TGC ATA      540
Tyr Cys Ser Gly His Cys Pro Asp Asp Ala Ile Asn Asn Thr Cys Ile
65          70          75
ACT AAT GGA CAT TGC TTT GCC ATC ATA GAA GAA GAT GAC CAG GGA GAA      588
Thr Asn Gly His Cys Phe Ala Ile Ile Glu Glu Asp Asp Gln Gly Glu
80          85          90
ACC ACA TTA GCT TCA GGG TGT ATG AAA TAT GAA GGA TCT GAT TTT CAG      636
Thr Thr Leu Ala Ser Gly Cys Met Lys Tyr Glu Gly Ser Asp Phe Gln
95          100          105
TGC AAA GAT TCT CCA AAA GCC CAG CTA CGC CGG ACA ATA GAA TGT TGT      684
Cys Lys Asp Ser Pro Lys Ala Gln Leu Arg Arg Thr Ile Glu Cys Cys
110          115          120          125
CGG ACC AAT TTA TGT AAC CAG TAT TTG CAA CCC ACA CTG CCC CCT GTT      732
Arg Thr Asn Leu Cys Asn Gln Tyr Leu Gln Pro Thr Leu Pro Pro Val
130          135          140
GTC ATA GGT CCG TTT TTT GAT GGC AGC ATT CGA TGG CTG GTT TTG CTC      780
Val Ile Gly Pro Phe Phe Asp Gly Ser Ile Arg Trp Leu Val Leu Leu
145          150          155
ATT TCT ATG GCT GTC TGC ATA ATT GCT ATG ATC ATC TTC TCC AGC TGC      828
Ile Ser Met Ala Val Cys Ile Ile Ala Met Ile Ile Phe Ser Ser Cys
160          165          170
TTT TGT TAC AAA CAT TAT TGC AAG AGC ATC TCA AGC AGA CGT CGT TAC      876
Phe Cys Tyr Lys His Tyr Cys Lys Ser Ile Ser Ser Arg Arg Arg Tyr
175          180          185
AAT CGT GAT TTG GAA CAG GAT GAA GCA TTT ATT CCA GTT GGA GAA TCA      924
Asn Arg Asp Leu Glu Gln Asp Glu Ala Phe Ile Pro Val Gly Glu Ser
190          195          200          205
CTA AAA GAC CTT ATT GAC CAG TCA CAA AGT TCT GGT AGT GGG TCT GGA      972
Leu Lys Asp Leu Ile Asp Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly
210          215          220
CTA CCT TTA TTG GTT CAG CGA ACT ATT GCC AAA CAG ATT CAG ATG GTC      1020
Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val
225          230          235
CGG CAA GTT GGT AAA GGC CGA TAT GGA GAA GTA TGG ATG GGC AAA TGG      1068
Arg Gln Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp
240          245          250
CGT GGC GAA AAA GTG GCG GTG AAA GTA TTC TTT ACC ACT GAA GAA GCC      1116
Arg Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala
255          260          265
AGC TGG TTT CGA GAA ACA GAA ATC TAC CAA ACT GTG CTA ATG CGC CAT      1164
Ser Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His
270          275          280          285
GAA AAC ATA CTT GGT TTC ATA GCG GCA GAC ATT AAA GGT ACA GGT TCC      1212
Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser
290          295          300
TGG ACT CAG CTC TAT TTG ATT ACT GAT TAC CAT GAA AAT GGA TCT CTC      1260
Trp Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu
305          310          315
TAT GAC TTC CTG AAA TGT GCT ACA CTG GAC ACC AGA GCC CTG CTT AAA      1308
Tyr Asp Phe Leu Lys Cys Ala Thr Leu Asp Thr Arg Ala Leu Leu Lys
320          325          330
TTG GCT TAT TCA GCT GCC TGT GGT CTG TGC CAC CTG CAC ACA GAA ATT      1356
Leu Ala Tyr Ser Ala Ala Cys Gly Leu Cys His Leu His Thr Glu Ile

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335	TAT GGC ACC CAA GGA AAG CCC GCA ATT GCT CAT CGA GAC CTA AAG AGC	1404
	Tyr Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser	
350	AAA AAC ATC CTC ATC AAG AAA AAT GGG AGT TGC TGC ATT GCT GAC CTG	1452
	Lys Asn Ile Leu Ile Lys Lys Asn Gly Ser Cys Cys Ile Ala Asp Leu	
	GGC CTT GCT GTT AAA TTC AAC AGT GAC ACA AAT GAA GTT GAT GTG CCC	1500
	Gly Leu Ala Val Lys Phe Asn Ser Asp Thr Asn Glu Val Asp Val Pro	
	TTG AAT ACC AGG GTG GGC ACC AAA CGC TAC ATG GCT CCC GAA GTG CTG	1548
	Leu Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu	
	GAC GAA AGC CTG AAC AAA AAC CAC TTC CAG CCC TAC ATC ATG GCT GAC	1596
	Asp Glu Ser Leu Asn Lys Asn His Phe Gln Pro Tyr Ile Met Ala Asp	
	ATC TAC AGC TTC GGC CTA ATC ATT TGG GAG ATG GCT CGT CGT TGT ATC	1644
	Ile Tyr Ser Phe Gly Leu Ile Ile Trp Glu Met Ala Arg Arg Cys Ile	
	ACA GGA GGG ATC GTG GAA GAA TAC CAA TTG CCA TAT TAC AAC ATG GTA	1692
	Thr Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr Tyr Asn Met Val	
	CCG AGT GAT CCG TCA TAC GAA GAT ATG CGT GAG GTT GTG TGT GTC AAA	1740
	Pro Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Val Val Cys Val Lys	
	CGT TTG CGG CCA ATT GTG TCT AAT CGG TGG AAC AGT GAT GAA TGT CTA	1788
	Arg Leu Arg Pro Ile Val Ser Asn Arg Trp Asn Ser Asp Glu Cys Leu	
	CGA GCA GTT TTG AAG CTA ATG TCA GAA TGC TGG GCC CAC AAT CCA GCC	1836
	Arg Ala Val Leu Lys Leu Met Ser Glu Cys Trp Ala His Asn Pro Ala	
	TCC AGA CTC ACA GCA TTG AGA ATT AAG AAG ACG CTT GCC AAG ATG GTT	1884
	Ser Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ala Lys Met Val	
	GAA TCC CAA GAT GTA AAA ATC TGATGGTTAA ACCATCGGAG GAGAAACTCT	1935
	Glu Ser Gln Asp Val Lys Ile	
530	AGACTGCAAG AACTGTTTTT ACCCATGGCA TGGGTGGAAT TAGAGTGGAA TAAGGATGTT	1995
	AACTTGGTTC TCAGACTCTT TCTTCACTAC GTGTTACAG GCTGCTAATA TTAAACCTTT	2055
	CAGTACTCTT ATTAGGATAC AAGCTGGGAA CTTCTAAACA CTTCAATCTT TATATATGGA	2115
	CAGCTTTATT TTAAATGTGG TTTTGTATGC CTTTTTTTAA GTGGGTTTTT ATGAACTGCA	2175
	TCAAGACTTC AATCCTGATT AGTGCTCCA GTCAAGCTCT GGGTACTGAA TTGCCTGTTC	2235
	ATAAAACGGT GCTTCTGTG AAAGCCTTAA GAAGATAAAT GAGCGCAGCA GAGATGGAGA	2295
	AATAGACTTT GCCTTTTACC TGAGACATTC AGTTCGTTTG TATTCTACCT TTGTAAAACA	2355
	GCCTATAGAT GATGATGTGT TTGGGATACT GCTTATTTTA TGATAGTTTG TCCTGTGTCC	2415
	TTAGTGATGT GTGTGTGTCT CCATGCACAT GCACGCCGGG ATTCCTCTGC TGCCATTTGA	2475
	ATTAGAAGAA AATAATTTAT ATGCATGCAC AGGAAGATAT TGGTGGCCGG TGGTTTTGTG	2535
	CTTTAAAAAT GCAATATCTG ACCAAGATTC GCCAATCTCA TACAAGCCAT TTACTTTGCA	2595
	AGTGAGATAG CTTCCCCACC AGCTTTATTT TTAAACATGA AAGCTGATGC CAAGGCCAAA	2655
	AGAAGTTTAA AGCATCTGTA AATTGGACT GTTTTCCTTC AACCACCATT TTTTTGTGG	2715
	TTATTATTTT TGTCACGGAA AGCATCCTCT CCAAAGTTGG AGCTTCTATT GCCATGAACC	2775
	ATGCTTACAA AGAAAGCACT TCTTATTGAA GTGAATTCCT GCATTTGATA GCAATGTAAG	2835
	TGCCTATAAC CATGTTCTAT ATTCTTTATT CTCAGTAACT TTTAAAAGGG AAGTTATTTA	2895
	TATTTGTGT ATAATGTGCT TTATTTGCAA ATCACCC	2932

(2) INFORMATION FOR SEQ ID NO: 6:

25402772.1

11

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 532 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

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Met Thr Gln Leu Tyr Ile Tyr Ile Arg Leu Leu Gly Ala Tyr Leu Phe
 1           5           10           15
Ile Ile Ser Arg Val Gln Gly Gln Asn Leu Asp Ser Met Leu His Gly
          20           25           30
Thr Gly Met Lys Ser Asp Ser Asp Gln Lys Lys Ser Glu Asn Gly Val
          35           40           45
Thr Leu Ala Pro Glu Asp Thr Leu Pro Phe Leu Lys Cys Tyr Cys Ser
          50           55           60
Gly His Cys Pro Asp Asp Ala Ile Asn Asn Thr Cys Ile Thr Asn Gly
          65           70           75           80
His Cys Phe Ala Ile Ile Glu Glu Asp Asp Gln Gly Glu Thr Thr Leu
          85           90           95
Ala Ser Gly Cys Met Lys Tyr Glu Gly Ser Asp Phe Gln Cys Lys Asp
          100          105          110
Ser Pro Lys Ala Gln Leu Arg Arg Thr Ile Glu Cys Cys Arg Thr Asn
          115          120          125
Leu Cys Asn Gln Tyr Leu Gln Pro Thr Leu Pro Pro Val Val Ile Gly
          130          135          140
Pro Phe Phe Asp Gly Ser Ile Arg Trp Leu Val Leu Leu Ile Ser Met
          145          150          155          160
Ala Val Cys Ile Ile Ala Met Ile Ile Phe Ser Ser Cys Phe Cys Tyr
          165          170          175
Lys His Tyr Cys Lys Ser Ile Ser Ser Arg Arg Arg Tyr Asn Arg Asp
          180          185          190
Leu Glu Gln Asp Glu Ala Phe Ile Pro Val Gly Glu Ser Leu Lys Asp
          195          200          205
Leu Ile Asp Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly Leu Pro Leu
          210          215          220
Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val Arg Gln Val
          225          230          235          240
Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp Arg Gly Glu
          245          250          255
Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala Ser Trp Phe
          260          265          270
Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His Glu Asn Ile
          275          280          285
Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser Trp Thr Gln
          290          295          300
Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu Tyr Asp Phe
          305          310          315          320
Leu Lys Cys Ala Thr Leu Asp Thr Arg Ala Leu Leu Lys Leu Ala Tyr
          325          330          335
Ser Ala Ala Cys Gly Leu Cys His Leu His Thr Glu Ile Tyr Gly Thr
          340          345          350
Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys Asn Ile
          355          360          365
Leu Ile Lys Lys Asn Gly Ser Cys Cys Ile Ala Asp Leu Gly Leu Ala
          370          375          380
Val Lys Phe Asn Ser Asp Thr Asn Glu Val Asp Val Pro Leu Asn Thr
          385          390          395          400
Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Ser

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          405          410          415
Leu Asn Lys Asn His Phe Gln Pro Tyr Ile Met Ala Asp Ile Tyr Ser
          420          425          430
Phe Gly Leu Ile Ile Trp Glu Met Ala Arg Arg Cys Ile Thr Gly Gly
          435          440          445
Ile Val Glu Glu Tyr Gln Leu Pro Tyr Tyr Asn Met Val Pro Ser Asp
          450          455          460
Pro Ser Tyr Glu Asp Met Arg Glu Val Val Cys Val Lys Arg Leu Arg
          465          470          475          480
Pro Ile Val Ser Asn Arg Trp Asn Ser Asp Glu Cys Leu Arg Ala Val
          485          490          495
Leu Lys Leu Met Ser Glu Cys Trp Ala His Asn Pro Ala Ser Arg Leu
          500          505          510
Thr Ala Leu Arg Ile Lys Lys Thr Leu Ala Lys Met Val Glu Ser Gln
          515          520          525
Asp Val Lys Ile
          530

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(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2333 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: CDS

- (B) LOCATION: 1..1515

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

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ATG GCG GAG TCG GCC GGA GCC TCC TCC TTC TTC CCC CTT GTT GTC CTC      48
Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu Val Val Leu
1          5          10          15
CTG CTC GCC GGC AGC GGC GGG TCC GGG CCC CGG GGG GTC CAG GCT CTG      96
Leu Leu Ala Gly Ser Gly Gly Ser Gly Pro Arg Gly Val Gln Ala Leu
          20          25          30
CTG TGT GCG TGC ACC AGC TGC CTC CAG GCC AAC TAC ACG TGT GAG ACA      144
Leu Cys Ala Cys Thr Ser Cys Leu Gln Ala Asn Tyr Thr Cys Glu Thr
          35          40          45
GAT GGG GCC TGC ATG GTT TCC TTT TTC AAT CTG GAT GGG ATG GAG CAC      192
Asp Gly Ala Cys Met Val Ser Phe Phe Asn Leu Asp Gly Met Glu His
          50          55          60
CAT GTG CGC ACC TGC ATC CCC AAA GTG GAG CTG GTC CCT GCC GGG AAG      240
His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro Ala Gly Lys
          65          70          75          80
CCC TTC TAC TGC CTG AGC TCG GAG GAC CTG CGC AAC ACC CAC TGC TGC      288
Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr His Cys Cys
          85          90          95
TAC ACT GAC TAC TGC AAC AGG ATC GAC TTG AGG GTG CCC AGT GGT CAC      336
Tyr Thr Asp Tyr Cys Asn Arg Ile Asp Leu Arg Val Pro Ser Gly His
          100          105          110
CTC AAG GAG CCT GAG CAC CCG TCC ATG TGG GGC CCG GTG GAG CTG GTA      384

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Leu Lys Glu Pro Glu His Pro Ser Met Trp Gly Pro Val Glu Leu Val	
115 120 125	
GGC ATC ATC GCC GGC CCG GTG TTC CTC CTG TTC CTC ATC ATC ATT	432
Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile Ile Ile Ile	
130 135 140	
GTT TTC CTT GTC ATT AAC TAT CAT CAG CGT GTC TAT CAC AAC CGC CAG	480
Val Phe Leu Val Ile Asn Tyr His Gln Arg Val Tyr His Asn Arg Gln	
145 150 155 160	
AGA CTG GAC ATG GAA GAT CCC TCA TGT GAG ATG TGT CTC TCC AAA GAC	528
Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met Cys Leu Ser Lys Asp	
165 170 175	
AAG ACG CTC CAG GAT CTT GTC TAC GAT CTC TCC ACC TCA GGG TCT GGC	576
Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser Thr Ser Gly Ser Gly	
180 185 190	
TCA GGG TTA CCC CTC TTT GTC CAG CGC ACA GTG GCC CGA ACC ATC GTT	624
Ser Gly Leu Pro Leu Phe Val Gln Arg Thr Val Ala Arg Thr Ile Val	
195 200 205	
TTA CAA GAG ATT ATT GGC AAG GGT CGG TTT GGG GAA GTA TGG CGG GGC	672
Leu Gln Glu Ile Ile Gly Lys Gly Arg Phe Gly Glu Val Trp Arg Gly	
210 215 220	
CGC TGG AGG GGT GGT GAT GTG GCT GTG AAA ATA TTC TCT TCT CGT GAA	720
Arg Trp Arg Gly Gly Asp Val Ala Val Lys Ile Phe Ser Ser Arg Glu	
225 230 235 240	
GAA CGG TCT TGG TTC AGG GAA GCA GAG ATA TAC CAG ACG GTC ATG CTG	768
Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr Val Met Leu	
245 250 255	
CGC CAT GAA AAC ATC CTT GGA TTT ATT GCT GCT GAC AAT AAA GAT AAT	816
Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn Lys Asp Asn	
260 265 270	
GGC ACC TGG ACA CAG CTG TGG CTT GTT TCT GAC TAT CAT GAG CAC GGG	864
Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His Glu His Gly	
275 280 285	
TCC CTG TTT GAT TAT CTG AAC CCG TAC ACA GTG ACA ATT GAG GGG ATG	912
Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Ile Glu Gly Met	
290 295 300	
ATT AAG CTG GCC TTG TCT GCT GCT AGT GGG CTG GCA CAC CTG CAC ATG	960
Ile Lys Leu Ala Leu Ser Ala Ala Ser Gly Leu Ala His Leu His Met	
305 310 315 320	
GAG ATC GTG GGC ACC CAA GGG AAG CCT GGA ATT GCT CAT CGA GAC TTA	1008
Glu Ile Val Gly Thr Gln Gly Lys Pro Gly Ile Ala His Arg Asp Leu	
325 330 335	
AAG TCA AAG AAC ATT CTG GTG AAG AAA AAT GGC ATG TGT GCC ATA GCA	1056
Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Met Cys Ala Ile Ala	
340 345 350	
GAC CTG GGC CTG GCT GTC CGT CAT GAT GCA GTC ACT GAC ACC ATT GAC	1104
Asp Leu Gly Leu Ala Val Arg His Asp Ala Val Thr Asp Thr Ile Asp	
355 360 365	
ATT GCC CCG AAT CAG AGG GTG GGG ACC AAA CGA TAC ATG GCC CCT GAA	1152
Ile Ala Pro Asn Gln Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu	
370 375 380	
GTA CTT GAT GAA ACC ATT AAT ATG AAA CAC TTT GAC TCC TTT AAA TGT	1200
Val Leu Asp Glu Thr Ile Asn Met Lys His Phe Asp Ser Phe Lys Cys	
385 390 395 400	
GCT GAT ATT TAT GCC CTC GGG CTT GTA TAT TGG GAG ATT GCT CGA AGA	1248
Ala Asp Ile Tyr Ala Leu Gly Leu Val Tyr Trp Glu Ile Ala Arg Arg	
405 410 415	
TGC AAT TCT GGA GGA GTC CAT GAA GAA TAT CAG CTG CCA TAT TAC GAC	1296

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Cys Asn Ser Gly Gly Val His Glu Glu Tyr Gln Leu Pro Tyr Tyr Asp
420 425 430
TTA GTG CCC TCT GAC CCT TCC ATT GAG GAA ATG CGA AAG GTT GTA TGT 1344
Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg Lys Val Val Cys
435 440 445
GAT CAG AAG CTG CGT CCC AAC ATC CCC AAC TGG TGG CAG AGT TAT GAG 1392
Asp Gln Lys Leu Arg Pro Asn Ile Pro Asn Trp Trp Gln Ser Tyr Glu
450 455 460
GCA CTG CCG GTG ATG GGG AAG ATG ATG CGA GAG TGT TGG TAT GCC AAC 1440
Ala Leu Arg Val Met Gly Lys Met Met Arg Glu Cys Trp Tyr Ala Asn
465 470 475 480
GGC GCA GCC CGC CTG ACG GCC CTG CGC ATC AAG AAG ACC CTC TCC CAG 1488
Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ser Gln
485 490 495
CTC AGC GTG CAG GAA GAC GTG AAG ATC TAACTGCTCC CTCTCTCCAC 1535
Leu Ser Val Gln Glu Asp Val Lys Ile
500 505
ACGGAGCTCC TGGCAGCGAG AACTACGCAC AGCTGCCGCG TTGAGCGTAC GATGGAGGCC 1595
TACCTCTCGT TTCTGCCAG CCCTCTGTGG CCAGGAGCCC TGGCCCGCAA GAGGGACAGA 1655
GCCCCGGAGA GACTCGCTCA CTCCCATGTT GGGTTTGAGA CAGACACCTT TTCTATTTAC 1715
CTCCTAATGG CATGGAGACT CTGAGAGCGA ATTGTGTGGA GAACTCAGTG CCACACCTCG 1775
AACTGGTTGT AGTGGGAAGT CCGCGAAAC CCGGTGCATC TGGCAGTGG CCAGGAGCCA 1835
TGACAGGGGC GCTTGGGAGG GGCCGGAGGA ACCGAGGTGT TGCCAGTGCT AAGCTGCCCT 1895
GAGGGTTTCC TTCGGGGACC AGCCCCACAGC ACACCAAGGT GGCCCGGAAG AACCAGAAGT 1955
GCAGCCCCCTC TCACAGGCAG CTCTGAGCCG CGCTTTCCCC TCCTCCCTGG GATGGACGCT 2015
GCCGGGAGAC TGCCAGTGGA GACGGAATCT GCCGCTTTGT CTGTCCAGCC GTGTGTGTCAT 2075
GTGCCGAGGT GCGTCCCCCG TTGTGCCCTGG TTCGTGCCAT GCCCTTACAC GTGCGTGTGA 2135
GTGTGTGTGT GTGTCTGTAG GTGCGCACTT ACCTGCTTGA GCTTTCTGTG CATGTGCAGG 2195
TCGGGGGTGT GGTCCGTCATG CTGTCCGTGC TTGCTGGTGC CTCTTTTCAG TAGTGAGCAG 2255
CATCTAGTTT CCCTGGTGCC CTTCCTGGA GGTCTCTCCC TCCCCAGAG CCCCTCATGC 2315
CACAGTGGTA CTCTGTGT 2333

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(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 505 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

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Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu Val Val Leu
1 5 10 15
Leu Leu Ala Gly Ser Gly Gly Ser Gly Pro Arg Gly Val Gln Ala Leu
20 25 30
Leu Cys Ala Cys Thr Ser Cys Leu Gln Ala Asn Tyr Thr Cys Glu Thr
35 40 45
Asp Gly Ala Cys Met Val Ser Phe Phe Asn Leu Asp Gly Met Glu His
50 55 60
His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro Ala Gly Lys
65 70 75 80
Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr His Cys Cys
85 90 95
Tyr Thr Asp Tyr Cys Asn Arg Ile Asp Leu Arg Val Pro Ser Gly His
100 105 110
Leu Lys Glu Pro Glu His Pro Ser Met Trp Gly Pro Val Glu Leu Val
115 120 125
Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile Ile Ile

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      130              135              140
Val Phe Leu Val Ile Asn Tyr His Gln Arg Val Tyr His Asn Arg Gln
145              150              155              160
Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met Cys Leu Ser Lys Asp
      165              170              175
Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser Thr Ser Gly Ser Gly
      180              185              190
Ser Gly Leu Pro Leu Phe Val Gln Arg Thr Val Ala Arg Thr Ile Val
      195              200              205
Leu Gln Glu Ile Ile Gly Lys Gly Arg Phe Gly Glu Val Trp Arg Gly
      210              215              220
Arg Trp Arg Gly Gly Asp Val Ala Val Lys Ile Phe Ser Ser Arg Glu
      225              230              235              240
Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr Val Met Leu
      245              250              255
Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn Lys Asp Asn
      260              265              270
Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His Glu His Gly
      275              280              285
Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Ile Glu Gly Met
      290              295              300
Ile Lys Leu Ala Leu Ser Ala Ala Ser Gly Leu Ala His Leu His Met
      305              310              315              320
Glu Ile Val Gly Thr Gln Gly Lys Pro Gly Ile Ala His Arg Asp Leu
      325              330              335
Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Met Cys Ala Ile Ala
      340              345              350
Asp Leu Gly Leu Ala Val Arg His Asp Ala Val Thr Asp Thr Ile Asp
      355              360              365
Ile Ala Pro Asn Gln Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu
      370              375              380
Val Leu Asp Glu Thr Ile Asn Met Lys His Phe Asp Ser Phe Lys Cys
      385              390              395              400
Ala Asp Ile Tyr Ala Leu Gly Leu Val Tyr Trp Glu Ile Ala Arg Arg
      405              410              415
Cys Asn Ser Gly Gly Val His Glu Glu Tyr Gln Leu Pro Tyr Tyr Asp
      420              425              430
Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg Lys Val Val Cys
      435              440              445
Asp Gln Lys Leu Arg Pro Asn Ile Pro Asn Trp Trp Gln Ser Tyr Glu
      450              455              460
Ala Leu Arg Val Met Gly Lys Met Met Arg Glu Cys Trp Tyr Ala Asn
      465              470              475              480
Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ser Gln
      485              490              495
Leu Ser Val Gln Glu Asp Val Lys Ile
      500              505

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(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2308 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 77..1585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

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GGCGAGGCCA GGTTTGCTGG GGTGAGGCAG CGGCGCGGCC GGGCCGGGCC GGGCCACAGG      60
CGGTGGCGGC GGGACC ATG GAG GCG GCG GTC GCT GCT CCG CGT CCC CGG      109
      Met Glu Ala Ala Val Ala Ala Pro Arg Pro Arg
              1              5              10
CTG CTC CTC CTC GTG CTG GCG GCG GCG GCG GCG GCG GCG GCG GCG CTG      157
Leu Leu Leu Leu Val Leu Ala Ala Ala Ala Ala Ala Ala Ala Leu
              15              20              25
CTC CCG GGG GCG ACG GCG TTA CAG TGT TTC TGC CAC CTC TGT ACA AAA      205
Leu Pro Gly Ala Thr Ala Leu Gln Cys Phe Cys His Leu Cys Thr Lys
              30              35              40
GAC AAT TTT ACT TGT GTG ACA GAT GGG CTC TGC TTT GTC TCT GTC ACA      253
Asp Asn Phe Thr Cys Val Thr Asp Gly Leu Cys Phe Val Ser Val Thr
              45              50              55
GAG ACC ACA GAC AAA GTT ATA CAC AAC AGC ATG TGT ATA GCT GAA ATT      301
Glu Thr Thr Asp Lys Val Ile His Asn Ser Met Cys Ile Ala Glu Ile
              60              65              70              75
GAC TTA ATT CCT CGA GAT AGG CCG TTT GTA TGT GCA CCC TCT TCA AAA      349
Asp Leu Ile Pro Arg Asp Arg Pro Phe Val Cys Ala Pro Ser Ser Lys
              80              85              90
ACT GGG TCT GTG ACT ACA ACA TAT TGC TGC AAT CAG GAC CAT TGC AAT      397
Thr Gly Ser Val Thr Thr Thr Tyr Cys Asn Gln Asp His Cys Asn
              95              100              105
AAA ATA GAA CTT CCA ACT ACT GTA AAG TCA TCA CCT GGC CTT GGT CCT      445
Lys Ile Glu Leu Pro Thr Thr Val Lys Ser Ser Pro Gly Leu Gly Pro
              110              115              120
GTG GAA CTG GCA GCT GTC ATT GCT GGA CCA GTG TGC TTC GTC TGC ATC      493
Val Glu Leu Ala Ala Val Ile Ala Gly Pro Val Cys Phe Val Cys Ile
              125              130              135
TCA CTC ATG TTG ATG GTC TAT ATC TGC CAC AAC CGC ACT GTC ATT CAC      541
Ser Leu Met Leu Met Val Tyr Ile Cys His Asn Arg Thr Val Ile His
              140              145              150              155
CAT CGA GTG CCA AAT GAA GAG GAC CCT TCA TTA GAT CGC CCT TTT ATT      589
His Arg Val Pro Asn Glu Glu Asp Pro Ser Leu Asp Arg Pro Phe Ile
              160              165              170
TCA GAG GGT ACT ACG TTG AAA GAC TTA ATT TAT GAT ATG ACA ACG TCA      637
Ser Glu Gly Thr Thr Leu Lys Asp Leu Ile Tyr Asp Met Thr Thr Ser
              175              180              185
GGT TCT GGC TCA GGT TTA CCA TTG CTT GTT CAG AGA ACA ATT GCG AGA      685
Gly Ser Gly Ser Gly Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Arg
              190              195              200
ACT ATT GTG TTA CAA GAA AGC ATT GGC AAA GGT CGA TTT GGA GAA GTT      733
Thr Ile Val Leu Gln Glu Ser Ile Gly Lys Gly Arg Phe Gly Glu Val
              205              210              215
TGG AGA GGA AAG TGG CGG GGA GAA GAA GTT GCT GTT AAG ATA TTC TCC      781
Trp Arg Gly Lys Trp Arg Gly Glu Glu Val Ala Val Lys Ile Phe Ser
              220              225              230              235
TCT AGA GAA GAA CGT TCG TGG TTC CGT GAG GCA GAG ATT TAT CAA ACT      829
Ser Arg Glu Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr
              240              245              250
GTA ATG TTA CGT CAT GAA AAC ATC CTG GGA TTT ATA GCA GCA GAC AAT      877

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Val Met Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn	
255 260 265	
AAA GAC AAT GGT ACT TGG ACT CAG CTC TGG TTG GTG TCA GAT TAT CAT	925
Lys Asp Asn Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His	
270 275 280	
GAG CAT GGA TCC CTT TTT GAT TAC TTA AAC AGA TAC ACA GTT ACT GTG	973
Glu His Gly Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Val	
285 290 295	
GAA GGA ATG ATA AAA CTT GCT CTG TCC ACG GCG AGC GGT CTT GCC CAT	1021
Glu Gly Met Ile Lys Leu Ala Leu Ser Thr Ala Ser Gly Leu Ala His	
300 305 310 315	
CTT CAC ATG GAG ATT GTT GGT ACC CAA GGA AAG CCA GCC ATT GCT CAT	1069
Leu His Met Glu Ile Val Gly Thr Gln Gly Lys Pro Ala Ile Ala His	
320 325 330	
AGA GAT TTG AAA TCA AAG AAT ATC TTG GTA AAG AAG AAT GGA ACT TGC	1117
Arg Asp Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Thr Cys	
335 340 345	
TGT ATT GCA GAC TTA GGA CTG GCA GTA AGA CAT GAT TCA GCC ACA GAT	1165
Cys Ile Ala Asp Leu Gly Leu Ala Val Arg His Asp Ser Ala Thr Asp	
350 355 360	
ACC ATT GAT ATT GCT CCA AAC CAC AGA GTG GGA ACA AAA AGG TAC ATG	1213
Thr Ile Asp Ile Ala Pro Asn His Arg Val Gly Thr Lys Arg Tyr Met	
365 370 375	
GCC CCT GAA GTT CTC GAT GAT TCC ATA AAT ATG AAA CAT TTT GAA TCC	1261
Ala Pro Glu Val Leu Asp Asp Ser Ile Asn Met Lys His Phe Glu Ser	
380 385 390 395	
TTC AAA CGT GCT GAC ATC TAT GCA ATG GGC TTA GTA TTC TGG GAA ATT	1309
Phe Lys Arg Ala Asp Ile Tyr Ala Met Gly Leu Val Phe Trp Glu Ile	
400 405 410	
GCT CGA CGA TGT TCC ATT GGT GGA ATT CAT GAA GAT TAC CAA CTG CCT	1357
Ala Arg Arg Cys Ser Ile Gly Gly Ile His Glu Asp Tyr Gln Leu Pro	
415 420 425	
TAT TAT GAT CTT GTA CCT TCT GAC CCA TCA GTT GAA GAA ATG AGA AAA	1405
Tyr Tyr Asp Leu Val Pro Ser Asp Pro Ser Val Glu Glu Met Arg Lys	
430 435 440	
GTT GTT TGT GAA CAG AAG TTA AGG CCA AAT ATC CCA AAC AGA TGG CAG	1453
Val Val Cys Glu Gln Lys Leu Arg Pro Asn Ile Pro Asn Arg Trp Gln	
445 450 455	
AGC TGT GAA GCC TTG AGA GTA ATG GCT AAA ATT ATG AGA GAA TGT TGG	1501
Ser Cys Glu Ala Leu Arg Val Met Ala Lys Ile Met Arg Glu Cys Trp	
460 465 470 475	
TAT GCC AAT GGA GCA GCT AGG CTT ACA GCA TTG CGG ATT AAG AAA ACA	1549
Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr	
480 485 490	
TTA TCG CAA CTC AGT CAA CAG GAA GGC ATC AAA ATG TAATTCTACA	1595
Leu Ser Gln Leu Ser Gln Gln Glu Gly Ile Lys Met	
495 500	
GCTTTGCCTG AACTCTCCTT TTTTCTTCAG ATCTGCTCCT GGGTTTTAAT TTGGGAGGTC	1655
AGTTGTTCTA CCTCACTGAG AGGGAACAGA AGGATATTGC TTCCTTTTGC AGCAGTGTA	1715
TAAAGTCAAT TAAAACTTC CCAGGATTTT TTTGGACCCA GGAAACAGCC ATGTGGGTCC	1775
TTTCTGTGCA CTATGAACGC TTCTTTCCCA GGACAGAAAA TGTGTAGTCT ACCTTTATTT	1835
TTTATTAACA AAACCTTGTTT TTTAAAAAGA TGATTGCTGG TCTTAACCTT AGGTAACCTT	1895
GCTGTGCTGG AGATCATCTT TAAGGGCAAA GGAGTTGGAT TGCTGAATTA CAATGAACAA	1955
TGTCTTATTA CTAAAGAAAG TGATTTACTC CTGGTTAGTA CATTCTCAGA GGATTCTGAA	2015
CCACTAGAGT TTCCTTGATT CAGACTTTGA ATGTACTGTT CTATAGTTT TCAGGATCTT	2075
AAAATAACA CTTATAAAAC TCTTATCTTG AGTCTAAAAA TGACCTCATA TAGTAGTGAG	2135
GAACATAATT CATGCAATTG TATTTTGTAT ACTATTATTG TTCTTTCACT TATTCAGAAC	2195

ATTACATGCC TTCAAAATGG GATTGTACTA TACCAGTAAG TGCCACTTCT GTGTCTTTCT 2255
 AATGGAAATG ACTAGAATTG CTGAAAGTCT CTATGTIAAA ACCTATAGTG TTT 2308

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 503 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Glu Ala Ala Val Ala Ala Pro Arg Pro Arg Leu Leu Leu Leu Val
 1 5 10 15
 Leu Ala Ala Ala Ala Ala Ala Ala Ala Leu Leu Pro Gly Ala Thr
 20 25 30
 Ala Leu Gln Cys Phe Cys His Leu Cys Thr Lys Asp Asn Phe Thr Cys
 35 40 45
 Val Thr Asp Gly Leu Cys Phe Val Ser Val Thr Glu Thr Thr Asp Lys
 50 55 60
 Val Ile His Asn Ser Met Cys Ile Ala Glu Ile Asp Leu Ile Pro Arg
 65 70 75 80
 Asp Arg Pro Phe Val Cys Ala Pro Ser Ser Lys Thr Gly Ser Val Thr
 85 90 95
 Thr Thr Tyr Cys Cys Asn Gln Asp His Cys Asn Lys Ile Glu Leu Pro
 100 105 110
 Thr Thr Val Lys Ser Ser Pro Gly Leu Gly Pro Val Glu Leu Ala Ala
 115 120 125
 Val Ile Ala Gly Pro Val Cys Phe Val Cys Ile Ser Leu Met Leu Met
 130 135 140
 Val Tyr Ile Cys His Asn Arg Thr Val Ile His His Arg Val Pro Asn
 145 150 155 160
 Glu Glu Asp Pro Ser Leu Asp Arg Pro Phe Ile Ser Glu Gly Thr Thr
 165 170 175
 Leu Lys Asp Leu Ile Tyr Asp Met Thr Thr Ser Gly Ser Gly Ser Gly
 180 185 190
 Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Arg Thr Ile Val Leu Gln
 195 200 205
 Glu Ser Ile Gly Lys Gly Arg Phe Gly Glu Val Trp Arg Gly Lys Trp
 210 215 220
 Arg Gly Glu Glu Val Ala Val Lys Ile Phe Ser Ser Arg Glu Glu Arg
 225 230 235 240
 Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr Val Met Leu Arg His
 245 250 255
 Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn Lys Asp Asn Gly Thr
 260 265 270
 Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His Glu His Gly Ser Leu
 275 280 285
 Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Val Glu Gly Met Ile Lys
 290 295 300
 Leu Ala Leu Ser Thr Ala Ser Gly Leu Ala His Leu His Met Glu Ile
 305 310 315 320
 Val Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser
 325 330 335
 Lys Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp Leu
 340 345 350
 Gly Leu Ala Val Arg His Asp Ser Ala Thr Asp Thr Ile Asp Ile Ala
 355 360 365

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Pro Asn His Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu
 370                      375                      380
Asp Asp Ser Ile Asn Met Lys His Phe Glu Ser Phe Lys Arg Ala Asp
385                      390                      395                      400
Ile Tyr Ala Met Gly Leu Val Phe Trp Glu Ile Ala Arg Arg Cys Ser
                      405                      410                      415
Ile Gly Gly Ile His Glu Asp Tyr Gln Leu Pro Tyr Tyr Asp Leu Val
                      420                      425                      430
Pro Ser Asp Pro Ser Val Glu Glu Met Arg Lys Val Val Cys Glu Gln
                      435                      440                      445
Lys Leu Arg Pro Asn Ile Pro Asn Arg Trp Gln Ser Cys Glu Ala Leu
                      450                      455                      460
Arg Val Met Ala Lys Ile Met Arg Glu Cys Trp Tyr Ala Asn Gly Ala
465                      470                      475                      480
Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ser Gln Leu Ser
                      485                      490                      495
Gln Gln Glu Gly Ile Lys Met
                      500

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(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1922 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 241..1746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

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GAGAGCACAG CCCTTCCCAG TCCCGGAGC CGCCGCGCCA CGCGCGCATG ATCAAGACCT      60
TTTCCCCGGC CCCACAGGGC CTCTGGACGT GAGACCCCGG CCGCCTCCGC AAGGAGAGGC      120
GGGGGTGAG TCGCCCTGTC CAAAGGCCTC AATCTAAACA ATCTTGATTC CTGTTGCCGG      180
CTGGCGGGAC CCGTAATGGC AGGAAATCTC ACCACATCTC TTCTCCTATC TCCAAGGACC      240
ATG ACC TTG GGG AGC TTC AGA AGG GGC CTT TTG ATG CTG TCG GTG GCC      288
Met Thr Leu Gly Ser Phe Arg Arg Gly Leu Met Leu Ser Val Ala
 1           5           10           15
TTG GGC CTA ACC CAG GGG AGA CTT GCG AAG CCT TCC AAG CTG GTG AAC      336
Leu Gly Leu Thr Gln Gly Arg Leu Ala Lys Pro Ser Lys Leu Val Asn
 20          25          30
TGC ACT TGT GAG AGC CCA CAC TGC AAG AGA CCA TTC TGC CAG GGG TCA      384
Cys Thr Cys Glu Ser Pro His Cys Lys Arg Pro Phe Cys Gln Gly Ser
 35          40          45
TGG TGC ACA GTG GTG CTG GTT CGA GAG CAG GGC AGG CAC CCC CAG GTC      432
Trp Cys Thr Val Val Leu Val Arg Glu Gln Gly Arg His Pro Gln Val
 50          55          60
TAT CGG GGC TGT GGG AGC CTG AAC CAG GAG CTC TGC TTG GGA CGT CCC      480
Tyr Arg Gly Cys Gly Ser Leu Asn Gln Glu Leu Cys Leu Gly Arg Pro
 65          70          75          80
ACG GAG TTT CTG AAC CAT CAC TGC TGC TAT AGA TCC TTC TGC AAC CAC      528
Thr Glu Phe Leu Asn His His Cys Cys Tyr Arg Ser Phe Cys Asn His

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	85	90	95	
AAC GTG TCT CTG ATG CTG GAG GCC ACC CAA ACT CCT TCG GAG GAG CCA				576
Asn Val Ser Leu Met Leu Glu Ala Thr Gln Thr Pro Ser Glu Glu Pro				
	100	105	110	
GAA GTT GAT GCC CAT CTG CCT CTG ATC CTG GGT CCT GTG CTG GCC TTG				624
Glu Val Asp Ala His Leu Pro Leu Ile Leu Gly Pro Val Leu Ala Leu				
	115	120	125	
CCG GTC CTG GTG GCC CTG GGT GCT CTG GGC TTG TGG CGT GTC CGG CGG				672
Pro Val Leu Val Ala Leu Gly Ala Leu Gly Leu Trp Arg Val Arg Arg				
	130	135	140	
AGG CAG GAG AAG CAG CGG GAT TTG CAC AGT GAC CTG GGC GAG TCC AGT				720
Arg Gln Glu Lys Gln Arg Asp Leu His Ser Asp Leu Gly Glu Ser Ser				
	145	150	155	160
CTC ATC CTG AAG GCA TCT GAA CAG GCA GAC AGC ATG TTG GGG GAC TTC				768
Leu Ile Leu Lys Ala Ser Glu Gln Ala Asp Ser Met Leu Gly Asp Phe				
	165	170	175	
CTG GAC AGC GAC TGT ACC ACG GGC AGC GGC TCG GGG CTC CCC TTC TTG				816
Leu Asp Ser Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe Leu				
	180	185	190	
GTG CAG AGG ACG GTA GCT CGG CAG GTT GCG CTG GTA GAG TGT GTG GGA				864
Val Gln Arg Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val Gly				
	195	200	205	
AAG GGC CGA TAT GGC GAG GTG TGG CGC GGT TCG TGG CAT GGC GAA AGC				912
Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Ser Trp His Gly Glu Ser				
	210	215	220	
GTG GCG GTC AAG ATT TTC TCC TCA CGA GAT GAG CAG TCC TGG TTC CGG				960
Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe Arg				
	225	230	235	240
GAG ACG GAG ATC TAC AAC ACA GTT CTG CTT AGA CAC GAC AAC ATC CTA				1008
Glu Thr Glu Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile Leu				
	245	250	255	
GGC TTC ATC GCC TCC GAC ATG ACT TCG CGG AAC TCG AGC ACG CAG CTG				1056
Gly Phe Ile Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln Leu				
	260	265	270	
TGG CTC ATC ACC CAC TAC CAT GAA CAC GGC TCC CTC TAT GAC TTT CTG				1104
Trp Leu Ile Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe Leu				
	275	280	285	
CAG AGG CAG ACG CTG GAG CCC CAG TTG GCC CTG AGG CTA GCT GTG TCC				1152
Gln Arg Gln Thr Leu Glu Pro Gln Leu Ala Leu Arg Leu Ala Val Ser				
	290	295	300	
CCG GCC TGC GGC CTG GCG CAC CTA CAT GTG GAG ATC TTT GGC ACT CAA				1200
Pro Ala Cys Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr Gln				
	305	310	315	320
GGC AAA CCA GCC ATT GCC CAT CGT GAC CTC AAG AGT CGC AAT GTG CTG				1248
Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Arg Asn Val Leu				
	325	330	335	
GTC AAG AGT AAC TTG CAG TGT TGC ATT GCA GAC CTG GGA CTG GCT GTG				1296
Val Lys Ser Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala Val				
	340	345	350	
ATG CAC TCA CAA AGC AAC GAG TAC CTG GAT ATC GGC AAC ACA CCC CGA				1344
Met His Ser Gln Ser Asn Glu Tyr Leu Asp Ile Gly Asn Thr Pro Arg				
	355	360	365	
GTG GGT ACC AAA AGA TAC ATG GCA CCC GAG GTG CTG GAT GAG CAC ATC				1392
Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu His Ile				
	370	375	380	
CGC ACA GAC TGC TTT GAG TCG TAC AAG TGG ACA GAC ATC TGG GCC TTT				1440
Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala Phe				

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385          390          395          400
GGC CTA GTG CTA TGG GAG ATC GCC CGG CGG ACC ATC ATC AAT GGC ATT      1488
Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Ile Asn Gly Ile
          405          410          415
GTG GAG GAT TAC AGG CCA CCT TTC TAT GAC ATG GTA CCC AAT GAC CCC      1536
Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Met Val Pro Asn Asp Pro
          420          425          430
AGT TTT GAG GAC ATG AAA AAG GTG GTG TGC GTT GAC CAG CAG ACA CCC      1584
Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro
          435          440          445
ACC ATC CCT AAC CGG CTG GCT GCA GAT CCG GTC CTC TCC GGG CTG GCC      1632
Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala
          450          455          460
CAG ATG ATG AGA GAG TGC TGG TAC CCC AAC CCC TCT GCT CGC CTC ACC      1680
Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr
          465          470          475          480
GCA CTG CGC ATA AAG AAG ACA TTG CAG AAG CTC AGT CAC AAT CCA GAG      1728
Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Leu Ser His Asn Pro Glu
          485          490          495
AAG CCC AAA GTG ATT CAC TAGCCCAGGG CCACCAGGCT TCCTCTGCCT      1776
Lys Pro Lys Val Ile His
          500
AAAGTGTGTG CTGGGGAAGA AGACATAGCC TGTCTGGGTA GAGGGAGTGA AGAGAGTGTG      1836
CACGCTGCCG TGTGTGTGCC TGCTCAGCTT GCTCCAGCC CATCCAGCCA AAAATACAGC      1896
TGAGCTGAAA TTCAAAAAA AAAAAA      1922

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(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 502 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

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Met Thr Leu Gly Ser Phe Arg Arg Gly Leu Leu Met Leu Ser Val Ala
 1          5          10          15
Leu Gly Leu Thr Gln Gly Arg Leu Ala Lys Pro Ser Lys Leu Val Asn
          20          25          30
Cys Thr Cys Glu Ser Pro His Cys Lys Arg Pro Phe Cys Gln Gly Ser
          35          40          45
Trp Cys Thr Val Val Leu Val Arg Glu Gln Gly Arg His Pro Gln Val
          50          55          60
Tyr Arg Gly Cys Gly Ser Leu Asn Gln Glu Leu Cys Leu Gly Arg Pro
          65          70          75          80
Thr Glu Phe Leu Asn His His Cys Cys Tyr Arg Ser Phe Cys Asn His
          85          90          95
Asn Val Ser Leu Met Leu Glu Ala Thr Gln Thr Pro Ser Glu Glu Pro
          100          105          110
Glu Val Asp Ala His Leu Pro Leu Ile Leu Gly Pro Val Leu Ala Leu
          115          120          125
Pro Val Leu Val Ala Leu Gly Ala Leu Gly Leu Trp Arg Val Arg Arg
          130          135          140
Arg Gln Glu Lys Gln Arg Asp Leu His Ser Asp Leu Gly Glu Ser Ser
          145          150          155          160
Leu Ile Leu Lys Ala Ser Glu Gln Ala Asp Ser Met Leu Gly Asp Phe
          165          170          175
Leu Asp Ser Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe Leu

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      180      185      190
Val Gln Arg Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val Gly
      195      200      205
Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Ser Trp His Gly Glu Ser
      210      215      220
Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe Arg
      225      230      235      240
Glu Thr Glu Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile Leu
      245      250      255
Gly Phe Ile Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln Leu
      260      265      270
Trp Leu Ile Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe Leu
      275      280      285
Gln Arg Gln Thr Leu Glu Pro Gln Leu Ala Leu Arg Leu Ala Val Ser
      290      295      300
Pro Ala Cys Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr Gln
      305      310      315      320
Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Arg Asn Val Leu
      325      330      335
Val Lys Ser Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala Val
      340      345      350
Met His Ser Gln Ser Asn Glu Tyr Leu Asp Ile Gly Asn Thr Pro Arg
      355      360      365
Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu His Ile
      370      375      380
Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala Phe
      385      390      395      400
Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Ile Asn Gly Ile
      405      410      415
Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Met Val Pro Asn Asp Pro
      420      425      430
Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro
      435      440      445
Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala
      450      455      460
Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr
      465      470      475      480
Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Leu Ser His Asn Pro Glu
      485      490      495
Lys Pro Lys Val Ile His
      500

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(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2070 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mouse

(ix) FEATURE:

- (A) NAME/KEY: CDS

(R) LOCATION: 217..1812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

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ATTCATGAGA TGAAGCATA GGTCAAAGCT GTTCGGAGAA ATTGGAACCTA CAGTTTTATC      60
TAGCCACATC TCTGAGAATT CTGAAGAAAG CAGCAGGTGA AAGTCATTGC CAAGTGATT      120
TGTTCTGTAA GGAAGCCTCC CTCATTCACT TACACCAGTG AGACAGCAGG ACCAGTCATT      180
CAAAGGGCCG TGTACAGGAC GCGTGCCAAT CAGACA ATG ACT CAG CTA TAC ACT      234
Met Thr Gln Leu Tyr Thr
1 5
TAC ATC AGA TTA CTG GGA GCC TGT CTG TTC ATC ATT TCT CAT GTT CAA      282
Tyr Ile Arg Leu Leu Gly Ala Cys Leu Phe Ile Ile Ser His Val Gln
10 15 20
GGG CAG AAT CTA GAT AGT ATG CTC CAT GGC ACT GGT ATG AAA TCA GAC      330
Gly Gln Asn Leu Asp Ser Met Leu His Gly Thr Gly Met Lys Ser Asp
25 30 35
TTG GAC CAG AAG AAG CCA GAA AAT GGA GTG ACT TTA GCA CCA GAG GAT      378
Leu Asp Gln Lys Lys Pro Glu Asn Gly Val Thr Leu Ala Pro Glu Asp
40 45 50
ACC TTG CCT TTC TTA AAG TGC TAT TGC TCA GGA CAC TGC CCA GAT GAT      426
Thr Leu Pro Phe Leu Lys Cys Tyr Cys Ser Gly His Cys Pro Asp Asp
55 60 65 70
GCT ATT AAT AAC ACA TGC ATA ACT AAT GGC CAT TGC TTT GCC ATT ATA      474
Ala Ile Asn Asn Thr Cys Ile Thr Asn Gly His Cys Phe Ala Ile Ile
75 80 85
GAA GAA GAT GAT CAG GGA GAA ACC ACA TTA ACT TCT GGG TGT ATG AAG      522
Glu Glu Asp Asp Gln Gly Glu Thr Thr Leu Thr Ser Gly Cys Met Lys
90 95 100
TAT GAA GGC TCT GAT TTT CAA TGC AAG GAT TCA CCG AAA GCC CAG CTA      570
Tyr Glu Gly Ser Asp Phe Gln Cys Lys Asp Ser Pro Lys Ala Gln Leu
105 110 115
CGC AGG ACA ATA GAA TGT TGT CGG ACC AAT TTG TGC AAC CAG TAT TTG      618
Arg Arg Thr Ile Glu Cys Cys Arg Thr Asn Leu Cys Asn Gln Tyr Leu
120 125 130
CAG CCT ACA CTG CCC CCT GTT GTT ATA GGT CCG TTC TTT GAT GGC AGC      666
Gln Pro Thr Leu Pro Pro Val Val Ile Gly Pro Phe Phe Asp Gly Ser
135 140 145 150
ATC CGA TGG CTG GTT GTG CTC ATT TCC ATG GCT GTC TGT ATA GTT GCT      714
Ile Arg Trp Leu Val Val Leu Ile Ser Met Ala Val Cys Ile Val Ala
155 160 165
ATG ATC ATC TTC TCC AGC TGC TTT TGC TAT AAG CAT TAT TGT AAG AGT      762
Met Ile Ile Phe Ser Ser Cys Phe Cys Tyr Lys His Tyr Cys Lys Ser
170 175 180
ATC TCA AGC AGG GGT CGT TAC AAC CGT GAT TTG GAA CAG GAT GAA GCA      810
Ile Ser Ser Arg Gly Arg Tyr Asn Arg Asp Leu Glu Gln Asp Glu Ala
185 190 195
TTT ATT CCA GTA GGA GAA TCA TTG AAA GAC CTG ATT GAC CAG TCC CAA      858
Phe Ile Pro Val Gly Glu Ser Leu Lys Asp Leu Ile Asp Gln Ser Gln
200 205 210
AGC TCT GGG AGT GGA TCT GGA TTG CCT TTA TTG GTT CAG CGA ACT ATT      906
Ser Ser Gly Ser Gly Ser Gly Leu Pro Leu Leu Val Gln Arg Thr Ile
215 220 225 230
GCC AAA CAG ATT CAG ATG GTT CGG CAG GTT GGT AAA GGC CGC TAT GGA      954
Ala Lys Gln Ile Gln Met Val Arg Gln Val Gly Lys Gly Arg Tyr Gly
235 240 245
GAA GTA TGG ATG GGT AAA TGG CGT GGT GAA AAA GTG GCT GTC AAA GTG      1002
Glu Val Trp Met Gly Lys Trp Arg Gly Glu Lys Val Ala Val Lys Val
250 255 260
TTT TTT ACC ACT GAA GAA GCT AGC TGG TTT AGA GAA ACA GAA ATC TAC      1050

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Phe Phe Thr Thr Glu Glu Ala Ser Trp Phe Arg Glu Thr Glu Ile Tyr	
265 270 275	
CAG ACG GTG TTA ATG CGT CAT GAA AAT ATA CTT GGT TTT ATA GCT GCA	1098
Gln Thr Val Leu Met Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala	
280 285 290	
GAC ATT AAA GGC ACT GGT TCC TGG ACT CAG CTG TAT TTG ATT ACT GAT	1146
Asp Ile Lys Gly Thr Gly Ser Trp Thr Gln Leu Tyr Leu Ile Thr Asp	
295 300 305 310	
TAC CAT GAA AAT GGA TCT CTC TAT GAC TTC CTG AAA TGT GCC ACA CTA	1194
Tyr His Glu Asn Gly Ser Leu Tyr Asp Phe Leu Lys Cys Ala Thr Leu	
315 320 325	
GAC ACC AGA GCC CTA CTC AAG TTA GCT TAT TCT GCT GCT TGT GGT CTG	1242
Asp Thr Arg Ala Leu Leu Lys Leu Ala Tyr Ser Ala Ala Cys Gly Leu	
330 335 340	
TGC CAC CTC CAC ACA GAA ATT TAT GGT ACC CAA GGG AAG CCT GCA ATT	1290
Cys His Leu His Thr Glu Ile Tyr Gly Thr Gln Gly Lys Pro Ala Ile	
345 350 355	
GCT CAT CGA GAC CTG AAG AGC AAA AAC ATC CTT ATT AAG AAA AAT GGA	1338
Ala His Arg Asp Leu Lys Ser Lys Asn Ile Leu Ile Lys Lys Asn Gly	
360 365 370	
AGT TGC TGT ATT GCT GAC CTG GGC CTA GCT GTT AAA TTC AAC AGT GAT	1386
Ser Cys Cys Ile Ala Asp Leu Gly Leu Ala Val Lys Phe Asn Ser Asp	
375 380 385 390	
ACA AAT GAA GTT GAC ATA CCC TTG AAT ACC AGG GTG GGC ACC AAG CGG	1434
Thr Asn Glu Val Asp Ile Pro Leu Asn Thr Arg Val Gly Thr Lys Arg	
395 400 405	
TAC ATG GCT CCA GAA GTG CTG GAT GAA AGC CTG AAT AAA AAC CAT TTC	1482
Tyr Met Ala Pro Glu Val Leu Asp Glu Ser Leu Asn Lys Asn His Phe	
410 415 420	
CAG CCC TAC ATC ATG GCT GAC ATC TAT AGC TTT GGT TTG ATC ATT TGG	1530
Gln Pro Tyr Ile Met Ala Asp Ile Tyr Ser Phe Gly Leu Ile Ile Trp	
425 430 435	
GAA ATG GCT CGT CGT TGT ATT ACA GGA GGA ATC GTG GAG GAA TAT CAA	1578
Glu Met Ala Arg Arg Cys Ile Thr Gly Gly Ile Val Glu Glu Tyr Gln	
440 445 450	
TTA CCA TAT TAC AAC ATG GTG CCC AGT GAC CCA TCC TAT GAG GAC ATG	1626
Leu Pro Tyr Tyr Asn Met Val Pro Ser Asp Pro Ser Tyr Glu Asp Met	
455 460 465 470	
CGT GAG GTT GTG TGT GTG AAA CGC TTG CGG CCA ATC GTG TCT AAC CGC	1674
Arg Glu Val Val Cys Val Lys Arg Leu Arg Pro Ile Val Ser Asn Arg	
475 480 485	
TGG AAC AGC GAT GAA TGT CTT CGA GCA GTT TTG AAG CTA ATG TCA GAA	1722
Trp Asn Ser Asp Glu Cys Leu Arg Ala Val Leu Lys Leu Met Ser Glu	
490 495 500	
TGT TGG GCC CAT AAT CCA GCC TCC AGA CTC ACA GCT TTG AGA ATC AAG	1770
Cys Trp Ala His Asn Pro Ala Ser Arg Leu Thr Ala Leu Arg Ile Lys	
505 510 515	
AAG ACA CTT GCA AAA ATG GTT GAA TCC CAG GAT GTA AAG ATT	1812
Lys Thr Leu Ala Lys Met Val Glu Ser Gln Asp Val Lys Ile	
520 525 530	
TGACAATTAA ACAATTTTGA GGGAGAATTT AGACTGCAAG AACTTCTTCA CCCAAGGAAT	1872
GGGTGGGATT AGCATGGAAT AGGATGTTGA CTGGTTTCC AGACTCCTC CTCTACATCT	1932
TCACAGGCTG CTAACAGTAA ACCTTACCGT ACTCTACAGA ATACAAGATT GGAACCTGGA	1992
ACTTCAAACA TGTCATTCTT TATATATGAC AGCTTTGTTT TAATGTGGGG TTTTTTTGTT	2052
TGCTTTTTTT GTTTTGTT	2070

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 532 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

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Met Thr Gln Leu Tyr Thr Tyr Ile Arg Leu Leu Gly Ala Cys Leu Phe
 1          5          10          15
Ile Ile Ser His Val Gln Gly Gln Asn Leu Asp Ser Met Leu His Gly
          20          25          30
Thr Gly Met Lys Ser Asp Leu Asp Gln Lys Lys Pro Glu Asn Gly Val
          35          40          45
Thr Leu Ala Pro Glu Asp Thr Leu Pro Phe Leu Lys Cys Tyr Cys Ser
          50          55          60
Gly His Cys Pro Asp Asp Ala Ile Asn Asn Thr Cys Ile Thr Asn Gly
          65          70          75          80
His Cys Phe Ala Ile Ile Glu Glu Asp Asp Gln Gly Glu Thr Thr Leu
          85          90          95
Thr Ser Gly Cys Met Lys Tyr Glu Gly Ser Asp Phe Gln Cys Lys Asp
          100          105          110
Ser Pro Lys Ala Gln Leu Arg Arg Thr Ile Glu Cys Cys Arg Thr Asn
          115          120          125
Leu Cys Asn Gln Tyr Leu Gln Pro Thr Leu Pro Pro Val Val Ile Gly
          130          135          140
Pro Phe Phe Asp Gly Ser Ile Arg Trp Leu Val Val Leu Ile Ser Met
          145          150          155          160
Ala Val Cys Ile Val Ala Met Ile Ile Phe Ser Ser Cys Phe Cys Tyr
          165          170          175
Lys His Tyr Cys Lys Ser Ile Ser Ser Arg Gly Arg Tyr Asn Arg Asp
          180          185          190
Leu Glu Gln Asp Glu Ala Phe Ile Pro Val Gly Glu Ser Leu Lys Asp
          195          200          205
Leu Ile Asp Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly Leu Pro Leu
          210          215          220
Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val Arg Gln Val
          225          230          235          240
Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp Arg Gly Glu
          245          250          255
Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala Ser Trp Phe
          260          265          270
Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His Glu Asn Ile
          275          280          285
Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser Trp Thr Gln
          290          295          300
Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu Tyr Asp Phe
          305          310          315          320
Leu Lys Cys Ala Thr Leu Asp Thr Arg Ala Leu Leu Lys Leu Ala Tyr
          325          330          335
Ser Ala Ala Cys Gly Leu Cys His Leu His Thr Glu Ile Tyr Gly Thr
          340          345          350
Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys Asn Ile
          355          360          365
Leu Ile Lys Lys Asn Gly Ser Cys Cys Ile Ala Asp Leu Gly Leu Ala
          370          375          380
Val Lys Phe Asn Ser Asp Thr Asn Glu Val Asp Ile Pro Leu Asn Thr
          385          390          395          400

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Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Ser
                        405                        410                        415
Leu Asn Lys Asn His Phe Gln Pro Tyr Ile Met Ala Asp Ile Tyr Ser
                        420                        425                        430
Phe Gly Leu Ile Ile Trp Glu Met Ala Arg Arg Cys Ile Thr Gly Gly
                        435                        440                        445
Ile Val Glu Glu Tyr Gln Leu Pro Tyr Tyr Asn Met Val Pro Ser Asp
                        450                        455                        460
Pro Ser Tyr Glu Asp Met Arg Glu Val Val Cys Val Lys Arg Leu Arg
465                        470                        475                        480
Pro Ile Val Ser Asn Arg Trp Asn Ser Asp Glu Cys Leu Arg Ala Val
                        485                        490                        495
Leu Lys Leu Met Ser Glu Cys Trp Ala His Asn Pro Ala Ser Arg Leu
                        500                        505                        510
Thr Ala Leu Arg Ile Lys Lys Thr Leu Ala Lys Met Val Glu Ser Gln
                        515                        520                        525
Asp Val Lys Ile
530

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(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mouse

(ix) FEATURE:

- (A) NAME/KEY: CDS

- (B) LOCATION: 10..1524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

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CGCGGTTAC ATG GCG GAG TCG GCC GGA GCC TCC TCC TTC TTC CCC CTT      48
Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu
      1              5              10
GTT GTC CTC CTG CTC GCC GGC AGC GGC GGG TCC GGG CCC CGG GGG ATC      96
Val Val Leu Leu Leu Ala Gly Ser Gly Gly Ser Gly Pro Arg Gly Ile
      15              20              25
CAG GCT CTG CTG TGT GCG TGC ACC AGC TGC CTA CAG ACC AAC TAC ACC      144
Gln Ala Leu Leu Cys Ala Cys Thr Ser Cys Leu Gln Thr Asn Tyr Thr
      30              35              40              45
TGT GAG ACA GAT GGG GCT TGC ATG GTC TCC ATC TTT AAC CTG GAT GGC      192
Cys Glu Thr Asp Gly Ala Cys Met Val Ser Ile Phe Asn Leu Asp Gly
      50              55              60
GTG GAG CAC CAT GTA CGT ACC TGC ATC CCC AAG GTG GAG CTG GTT CCT      240
Val Glu His His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro
      65              70              75
GCT GGA AAG CCC TTC TAC TGC CTG AGT TCA GAG GAT CTG CGC AAC ACA      288
Ala Gly Lys Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr
      80              85              90
CAC TGC TGC TAT ATT GAC TTC TGC AAC AAG ATT GAC CTC AGG GTC CCC      336
His Cys Cys Tyr Ile Asp Phe Cys Asn Lys Ile Asp Leu Arg Val Pro
      95              100              105

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AGC GGA CAC CTC AAG GAG CCT GCG CAC CCC TCC ATG TGG GGC CCT GTG      384
Ser Gly His Leu Lys Glu Pro Ala His Pro Ser Met Trp Gly Pro Val
110      115      120      125
GAG CTG GTC GGC ATC ATC GCC GGC CCC GTC TTC CTC CTC TTC CTT ATC      432
Glu Leu Val Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile
130      135      140
ATT ATC ATC GTC TTC CTG GTC ATC AAC TAT CAC CAG CGT GTC TAC CAT      480
Ile Ile Ile Val Phe Leu Val Ile Asn Tyr His Gln Arg Val Tyr His
145      150      155
AAC CGC CAG AGG TTG GAC ATG GAG GAC CCC TCT TGC GAG ATG TGT CTC      528
Asn Arg Gln Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met Cys Leu
160      165      170
TCC AAA GAC AAG ACG CTC CAG GAT CTC GTC TAC GAC CTC TCC ACG TCA      576
Ser Lys Asp Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser Thr Ser
175      180      185
GGG TCT GGC TCA GGG TTA CCC CTT TTT GTC CAG CGC ACA GTG GCC CGA      624
Gly Ser Gly Ser Gly Leu Pro Leu Phe Val Gln Arg Thr Val Ala Arg
190      195      200      205
ACC ATT GTT TTA CAA GAG ATT ATC GGC AAG GGC CGG TTC GGG GAA GTA      672
Thr Ile Val Leu Gln Glu Ile Ile Gly Lys Gly Arg Phe Gly Glu Val
210      215      220
TGG CGT GGT CGC TGG AGG GGT GGT GAC GTG GCT GTG AAA ATC TTC TCT      720
Trp Arg Gly Arg Trp Arg Gly Gly Asp Val Ala Val Lys Ile Phe Ser
225      230      235
TCT CGT GAA GAA CGG TCT TGG TTC CGT GAA GCA GAG ATC TAC CAG ACC      768
Ser Arg Glu Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr
240      245      250
GTC ATG CTG CGC CAT GAA AAC ATC CTT GGC TTT ATT GCT GCT GAC AAT      816
Val Met Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn
255      260      265
AAA GAT AAT GGC ACC TGG ACC CAG CTG TGG CTT GTC TCT GAC TAT CAC      864
Lys Asp Asn Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His
270      275      280      285
GAG CAT GGC TCA CTG TTT GAT TAT CTG AAC CGC TAC ACA GTG ACC ATT      912
Glu His Gly Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Ile
290      295      300
GAG GGA ATG ATT AAG CTA GCC TTG TCT GCA GCC AGT GGT TTG GCA CAC      960
Glu Gly Met Ile Lys Leu Ala Leu Ser Ala Ala Ser Gly Leu Ala His
305      310      315
CTG CAT ATG GAG ATT GTG GGC ACT CAA GGG AAG CCG GGA ATT GCT CAT      1008
Leu His Met Glu Ile Val Gly Thr Gln Gly Lys Pro Gly Ile Ala His
320      325      330
CGA GAC TTG AAG TCA AAG AAC ATC CTG GTG AAA AAA AAT GGC ATG TGT      1056
Arg Asp Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Met Cys
335      340      345
GCC ATT GCA GAC CTG GGC CTG GCT GTC CGT CAT GAT GCG GTC ACT GAC      1104
Ala Ile Ala Asp Leu Gly Leu Ala Val Arg His Asp Ala Val Thr Asp
350      355      360      365
ACC ATA GAC ATT GCT CCA AAT CAG AGG GTG GGG ACC AAA CGA TAC ATG      1152
Thr Ile Asp Ile Ala Pro Asn Gln Arg Val Gly Thr Lys Arg Tyr Met
370      375      380
GCT CCT GAA GTC CTT GAC GAG ACA ATC AAC ATG AAG CAC TTT GAC TCC      1200
Ala Pro Glu Val Leu Asp Glu Thr Ile Asn Met Lys His Phe Asp Ser
385      390      395
TTC AAA TGT GCC GAC ATC TAT GCC CTC GGG CTT GTC TAC TGG GAG ATT      1248
Phe Lys Cys Ala Asp Ile Tyr Ala Leu Gly Leu Val Tyr Trp Glu Ile
400      405      410

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GCA CGA AGA TGC AAT TCT GGA GGA GTC CAT GAA GAC TAT CAA CTG CCG	1296
Ala Arg Arg Cys Asn Ser Gly Gly Val His Glu Asp Tyr Gln Leu Pro	
415 420 425	
TAT TAC GAC TTA GTG CCC TCC GAC CCT TCC ATT GAG GAG ATG CGA AAG	1344
Tyr Tyr Asp Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg Lys	
430 435 440 445	
GTT GTA TGT GAC CAG AAG CTA CGG CCC AAT GTC CCC AAC TGG TGG CAG	1392
Val Val Cys Asp Gln Lys Leu Arg Pro Asn Val Pro Asn Trp Trp Gln	
450 455 460	
AGT TAT GAG GCC TTG CGA GTG ATG GGA AAG ATG ATG CGG GAG TGC TGG	1440
Ser Tyr Glu Ala Leu Arg Val Met Gly Lys Met Met Arg Glu Cys Trp	
465 470 475	
TAC GCC AAT GGT GCT GCC CGT CTG ACA GCT CTG CGC ATC AAG AAG ACT	1488
Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr	
480 485 490	
CTG TCC CAG CTA AGC GTG CAG GAA GAT GTG AAG ATT TAAGCTGTTC	1534
Leu Ser Gln Leu Ser Val Gln Glu Asp Val Lys Ile	
495 500 505	
CTCTGCCTAC ACAAAGAACC TGGGCAGTGA GGATGACTGC AGCCACCGTG CAAGCGTCGT	1594
GGAGGCCTAT CCTCTTGTTT CTGCCCCGCC CTCTGGCAGA GCCCTGGCCT GCAAGAGGGA	1654
CAGAGCCTGG GAGACGCGCG CACTCCCCTT GGGTTTGAGA CAGACACTTT TTATATTTAC	1714
CTCCTGATGG CATGGAGACC TGAGCAAATC ATGTAGTCAC TCAATGCCAC AACTCAAAC	1774
GCTTCAGTGG GAAGTACAGA GACCCAGTGC ATTGCGTGTG CAGGAGCGTG AGGTGCTGGG	1834
CTCGCCAGGA GCGGCCCCCA TACCTTGTTG TCCACTGGGC TGCAGGTTTT CCTCCAGGGA	1894
CCAGTCAACT GGCATCAAGA TATTGAGAGG AACCGGAAGT TTCTCCCTCC TTCCCGTAGC	1954
AGTCCTGAGC CACACCATCC TTCTCATGGA CATCCGGAGG ACTGCCCTTA GAGACACAAC	2014
CTGCTGCCTG TCTGTCCAGC CAAGTGCGCA TGTGCCGAGG TGTGTCCAC ATTGTGCCTG	2074
GTCTGTGCCA CCGCCGTGTG TGTGTGTGTG TGTGTGAGTG AGTGTGTGTG TGTACACTTA	2134
ACCTGCTTCA GCTTCTGTGC ATGTGT	2160

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 505 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Met	Ala	Glu	Ser	Ala	Gly	Ala	Ser	Ser	Phe	Phe	Pro	Leu	Val	Val	Leu
1				5					10					15	
Leu	Leu	Ala	Gly	Ser	Gly	Gly	Ser	Gly	Pro	Arg	Gly	Ile	Gln	Ala	Leu
		20						25					30		
Leu	Cys	Ala	Cys	Thr	Ser	Cys	Leu	Gln	Thr	Asn	Tyr	Thr	Cys	Glu	Thr
		35					40					45			
Asp	Gly	Ala	Cys	Met	Val	Ser	Ile	Phe	Asn	Leu	Asp	Gly	Val	Glu	His
		50				55				60					
His	Val	Arg	Thr	Cys	Ile	Pro	Lys	Val	Glu	Leu	Val	Pro	Ala	Gly	Lys
		65			70				75				80		
Pro	Phe	Tyr	Cys	Leu	Ser	Ser	Glu	Asp	Leu	Arg	Asn	Thr	His	Cys	Cys
			85				90					95			
Tyr	Ile	Asp	Phe	Cys	Asn	Lys	Ile	Asp	Leu	Arg	Val	Pro	Ser	Gly	His
		100				105						110			
Leu	Lys	Glu	Pro	Ala	His	Pro	Ser	Met	Trp	Gly	Pro	Val	Glu	Leu	Val
		115				120					125				
Gly	Ile	Ile	Ala	Gly	Pro	Val	Phe	Leu	Leu	Phe	Leu	Ile	Ile	Ile	Ile
	130				135				140						
Val	Phe	Leu	Val	Ile	Asn	Tyr	His	Gln	Arg	Val	Tyr	His	Asn	Arg	Gln

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145          150          155          160
Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met Cys Leu Ser Lys Asp
          165          170          175
Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser Thr Ser Gly Ser Gly
          180          185          190
Ser Gly Leu Pro Leu Phe Val Gln Arg Thr Val Ala Arg Thr Ile Val
          195          200          205
Leu Gln Glu Ile Ile Gly Lys Gly Arg Phe Gly Glu Val Trp Arg Gly
          210          215          220
Arg Trp Arg Gly Gly Asp Val Ala Val Lys Ile Phe Ser Ser Arg Glu
225          230          235          240
Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr Val Met Leu
          245          250          255
Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn Lys Asp Asn
          260          265          270
Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His Glu His Gly
          275          280          285
Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Ile Glu Gly Met
290          295          300
Ile Lys Leu Ala Leu Ser Ala Ala Ser Gly Leu Ala His Leu His Met
305          310          315          320
Glu Ile Val Gly Thr Gln Gly Lys Pro Gly Ile Ala His Arg Asp Leu
          325          330          335
Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Met Cys Ala Ile Ala
          340          345          350
Asp Leu Gly Leu Ala Val Arg His Asp Ala Val Thr Asp Thr Ile Asp
          355          360          365
Ile Ala Pro Asn Gln Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu
          370          375          380
Val Leu Asp Glu Thr Ile Asn Met Lys His Phe Asp Ser Phe Lys Cys
385          390          395          400
Ala Asp Ile Tyr Ala Leu Gly Leu Val Tyr Trp Glu Ile Ala Arg Arg
          405          410          415
Cys Asn Ser Gly Gly Val His Glu Asp Tyr Gln Leu Pro Tyr Tyr Asp
          420          425          430
Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg Lys Val Val Cys
          435          440          445
Asp Gln Lys Leu Arg Pro Asn Val Pro Asn Trp Trp Gln Ser Tyr Glu
          450          455          460
Ala Leu Arg Val Met Gly Lys Met Met Arg Glu Cys Trp Tyr Ala Asn
465          470          475          480
Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ser Gln
          485          490          495
Leu Ser Val Gln Glu Asp Val Lys Ile
          500          505

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(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1952 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 187..1692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

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AAGCGGCGGC AGAAGTTGCC GCGTGGTGC TCGTAGTGAG GGCGCGGAGG ACCCGGGACC      60
TGGGAAGCGG CGGCGGGTTA ACTTCGGCTG AATCACAACC ATTTGGCGCT GAGCTATGAC      120
AAGAGAGCAA ACAAAAAGTT AAAGGAGCAA CCCGGCCATA AGTGAAGAGA GAAGTTTATT      180
GATAAC ATG CTC TTA CGA AGC TCT GGA AAA TTA AAT GTG GGC ACC AAG      228
Met Leu Leu Arg Ser Ser Gly Lys Leu Asn Val Gly Thr Lys
   1             5             10
AAG GAG GAT GGA GAG AGT ACA GCC CCC ACC CCT CGG CCC AAG ATC CTA      276
Lys Glu Asp Gly Glu Ser Thr Ala Pro Thr Pro Arg Pro Lys Ile Leu
   15             20             25             30
CGT TGT AAA TGC CAC CAC CAC TGT CCG GAA GAC TCA GTC AAC AAT ATC      324
Arg Cys Lys Cys His His His Cys Pro Glu Asp Ser Val Asn Asn Ile
           35             40             45
TGC AGC ACA GAT GGG TAC TGC TTC ACG ATG ATA GAA GAA GAT GAC TCT      372
Cys Ser Thr Asp Gly Tyr Cys Phe Thr Met Ile Glu Glu Asp Asp Ser
           50             55             60
GGA ATG CCT GTT GTC ACC TCT GGA TGT CTA GGA CTA GAA GGG TCA GAT      420
Gly Met Pro Val Val Thr Ser Gly Cys Leu Gly Leu Glu Gly Ser Asp
           65             70             75
TTT CAA TGT CGT GAC ACT CCC ATT OCT CAT CAA AGA AGA TCA ATT GAA      468
Phe Gln Cys Arg Asp Thr Pro Ile Pro His Gln Arg Arg Ser Ile Glu
           80             85             90
TGC TGC ACA GAA AGG AAT GAG TGT AAT AAA GAC CTC CAC CCC ACT CTG      516
Cys Cys Thr Glu Arg Asn Glu Cys Asn Lys Asp Leu His Pro Thr Leu
           95             100             105             110
CCT CCT CTC AAG GAC AGA GAT TTT GTT GAT GGG CCC ATA CAC CAC AAG      564
Pro Pro Leu Lys Asp Arg Asp Phe Val Asp Gly Pro Ile His His Lys
           115             120             125
GCC TTG CTT ATC TCT GTG ACT GTC TGT AGT TTA CTC TTG GTC CTC ATT      612
Ala Leu Leu Ile Ser Val Thr Val Cys Ser Leu Leu Leu Val Leu Ile
           130             135             140
ATT TTA TTC TGT TAC TTC AGG TAT AAA AGA CAA GAA GCC CGA CCT CGG      660
Ile Leu Phe Cys Tyr Phe Arg Tyr Lys Arg Gln Glu Ala Arg Pro Arg
           145             150             155
TAC AGC ATT GGG CTG GAG CAG GAC GAG ACA TAC ATT CCT CCT GGA GAG      708
Tyr Ser Ile Gly Leu Glu Gln Asp Glu Thr Tyr Ile Pro Pro Gly Glu
           160             165             170
TCC CTG AGA GAC TTG ATC GAG CAG TCT CAG AGC TCG GGA AGT GGA TCA      756
Ser Leu Arg Asp Leu Ile Glu Gln Ser Gln Ser Ser Gly Ser Gly Ser
           175             180             185             190
GGC CTC CCT CTG CTG GTC CAA AGG ACA ATA GCT AAG CAA ATT CAG ATG      804
Gly Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met
           195             200             205
GTG AAG CAG ATT GGA AAA GGC CGC TAT GGC GAG GTG TGG ATG GGA AAG      852
Val Lys Gln Ile Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys
           210             215             220
TGG CGT GGA GAA AAG GTG GCT GTG AAA GTG TTC TTC ACC ACG GAG GAA      900
Trp Arg Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu
           225             230             235
GCC AGC TGG TTC CGA GAG ACT GAG ATA TAT CAG ACG GTC CTG ATG CGG      948
Ala Ser Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg
           240             245             250

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CAT GAG AAT ATT CTG GGG TTC ATT GCT GCA GAT ATC AAA GGG ACT GGG	996
His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly	
255 260 265 270	
TCC TGG ACT CAG TTG TAC CTC ATC ACA GAC TAT CAT GAA AAC GGC TCC	1044
Ser Trp Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser	
275 280 285	
CTT TAT GAC TAT CTG AAA TCC ACC ACC TTA GAC GCA AAG TCC ATG CTG	1092
Leu Tyr Asp Tyr Leu Lys Ser Thr Thr Leu Asp Ala Lys Ser Met Leu	
290 295 300	
AAG CTA GCC TAC TCC TCT GTC AGC GGC CTA TGC CAT TTA CAC ACG GAA	1140
Lys Leu Ala Tyr Ser Ser Val Ser Gly Leu Cys His Leu His Thr Glu	
305 310 315	
ATC TTT AGC ACT CAA GGC AAG CCA GCA ATC GCC CAT CGA GAC TTG AAA	1188
Ile Phe Ser Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys	
320 325 330	
AGT AAA AAC ATC CTG GTG AAG AAA AAT GGA ACT TGC TGC ATA GCA GAC	1236
Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp	
335 340 345 350	
CTG GGC TTG GCT GTC AAG TTC ATT AGT GAC ACA AAT GAG GTT GAC ATC	1284
Leu Gly Leu Ala Val Lys Phe Ile Ser Asp Thr Asn Glu Val Asp Ile	
355 360 365	
CCA CCC AAC ACC CGG GTT GGC ACC AAG CGC TAT ATG CCT CCA GAA GTG	1332
Pro Pro Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Pro Pro Glu Val	
370 375 380	
CTG GAC GAG AGC TTG AAT AGA AAC CAT TTC CAG TCC TAC ATT ATG GCT	1380
Leu Asp Glu Ser Leu Asn Arg Asn His Phe Gln Ser Tyr Ile Met Ala	
385 390 395	
GAC ATG TAC AGC TTT GGA CTC ATC CTC TGG GAG ATT GCA AGG AGA TGT	1428
Asp Met Tyr Ser Phe Gly Leu Ile Leu Trp Glu Ile Ala Arg Arg Cys	
400 405 410	
GTT TCT GGA GGT ATA GTG GAA GAA TAC CAG CTT CCC TAT CAC GAC CTG	1476
Val Ser Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr His Asp Leu	
415 420 425 430	
GTG CCC AGT GAC CCT TCT TAT GAG GAC ATG AGA GAA ATT GTG TGC ATG	1524
Val Pro Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Ile Val Cys Met	
435 440 445	
AAG AAG TTA CGG CCT TCA TTC CCC AAT CGA TGG AGC AGT GAT GAG TGT	1572
Lys Lys Leu Arg Pro Ser Phe Pro Asn Arg Trp Ser Ser Asp Glu Cys	
450 455 460	
CTC AGG CAG ATG GGG AAG CTT ATG ACA GAG TGC TGG GCG CAG AAT CCT	1620
Leu Arg Gln Met Gly Lys Leu Met Thr Glu Cys Trp Ala Gln Asn Pro	
465 470 475	
GCC TCC AGG CTG ACG GCC CTG AGA GTT AAG AAA ACC CTT GCC AAA ATG	1668
Ala Ser Arg Leu Thr Ala Leu Arg Val Lys Lys Thr Leu Ala Lys Met	
480 485 490	
TCA GAG TCC CAG GAC ATT AAA CTC TGACGTCAGA TACTTGTGGA CAGAGCAAGA	1722
Ser Glu Ser Gln Asp Ile Lys Leu	
495 500	
ATTTCACAGA AGCATCGTTA GCGCAAGCCT TGAACGTTAG CCTACTGCCC AGTGAGTTCA	1782
GACTTTCCTG GAAGAGAGCA CGGTGGGCAG ACACAGAGGA ACCCAGAAAC ACGGATTCAT	1842
CATGGCTTTC TGAGGAGGAG AACTGTTTG GGTAACCTGT TCAAGATATG ATGCATGTTG	1902
CTTCTAAGA AAGCCCTGTA TTTTGAATTA CCATTTTTTT ATAAAAAAA	1952

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 502 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

```

Met Leu Leu Arg Ser Ser Gly Lys Leu Asn Val Gly Thr Lys Lys Glu
 1      5      10      15
Asp Gly Glu Ser Thr Ala Pro Thr Pro Arg Pro Lys Ile Leu Arg Cys
 20      25      30
Lys Cys His His His Cys Pro Glu Asp Ser Val Asn Asn Ile Cys Ser
 35      40      45
Thr Asp Gly Tyr Cys Phe Thr Met Ile Glu Glu Asp Asp Ser Gly Met
 50      55      60
Pro Val Val Thr Ser Gly Cys Leu Gly Leu Glu Gly Ser Asp Phe Gln
 65      70      75      80
Cys Arg Asp Thr Pro Ile Pro His Gln Arg Arg Ser Ile Glu Cys Cys
 85      90      95
Thr Glu Arg Asn Glu Cys Asn Lys Asp Leu His Pro Thr Leu Pro Pro
 100     105     110
Leu Lys Asp Arg Asp Phe Val Asp Gly Pro Ile His His Lys Ala Leu
 115     120     125
Leu Ile Ser Val Thr Val Cys Ser Leu Leu Leu Val Leu Ile Ile Leu
 130     135     140
Phe Cys Tyr Phe Arg Tyr Lys Arg Gln Glu Ala Arg Pro Arg Tyr Ser
 145     150     155     160
Ile Gly Leu Glu Gln Asp Glu Thr Tyr Ile Pro Pro Gly Glu Ser Leu
 165     170     175
Arg Asp Leu Ile Glu Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly Leu
 180     185     190
Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val Lys
 195     200     205
Gln Ile Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp Arg
 210     215     220
Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala Ser
 225     230     235     240
Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His Glu
 245     250     255
Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser Trp
 260     265     270
Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu Tyr
 275     280     285
Asp Tyr Leu Lys Ser Thr Thr Leu Asp Ala Lys Ser Met Leu Lys Leu
 290     295     300
Ala Tyr Ser Ser Val Ser Gly Leu Cys His Leu His Thr Glu Ile Phe
 305     310     315     320
Ser Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys
 325     330     335
Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp Leu Gly
 340     345     350
Leu Ala Val Lys Phe Ile Ser Asp Thr Asn Glu Val Asp Ile Pro Pro
 355     360     365
Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Pro Pro Glu Val Leu Asp
 370     375     380
Glu Ser Leu Asn Arg Asn His Phe Gln Ser Tyr Ile Met Ala Asp Met
 385     390     395     400
Tyr Ser Phe Gly Leu Ile Leu Trp Glu Ile Ala Arg Arg Cys Val Ser
 405     410     415
Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr His Asp Leu Val Pro

```

```

          420                      425                      430
Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Ile Val Cys Met Lys Lys
          435                      440                      445
Leu Arg Pro Ser Phe Pro Asn Arg Trp Ser Ser Asp Glu Cys Leu Arg
          450                      455                      460
Gln Met Gly Lys Leu Met Thr Glu Cys Trp Ala Gln Asn Pro Ala Ser
          465                      470                      475                      480
Arg Leu Thr Ala Leu Arg Val Lys Lys Thr Leu Ala Lys Met Ser Glu
          485                      490                      495
Ser Gln Asp Ile Lys Leu
          500

```

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GCGGATCCTG TTGTGAAGGN AATATGTG

28

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GCGATCCGTC GCAGTCAAAA TTTT

24

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GCGGATCCGC GATATATTAA AAGCAA

26

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: YES
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:
CGGAATTCTG GTGCCATATA

20

(2) INFORMATION FOR SEQ ID NO: 23:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:
ATTCAAGGGC ACATCAACTT CATTTGTGTC ACTGTTG

37

(2) INFORMATION FOR SEQ ID NO: 24:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:
GCGGATCCAC CATGGCGGAG TCGGCC

26

(2) INFORMATION FOR SEQ ID NO: 25:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:
AACACCGGGC CGGCGATGAT

20

(2) INFORMATION FOR SEQ ID NO: 26:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(v) FRAGMENT TYPE: internal
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:
Gly Xaa Gly Xaa Xaa Gly
1 5

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Asp Phe Lys Ser Arg Asn
 1 5

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Asp Leu Lys Ser Lys Asn
 1 5

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Gly Thr Lys Arg Tyr Met
 1 5

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 513 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Met	Gly	Ala	Ala	Ala	Lys	Leu	Ala	Phe	Ala	Val	Phe	Leu	Ile	Ser	Cys	5	10	15
Ser	Ser	Gly	Ala	Ile	Leu	Gly	Arg	Ser	Glu	Thr	Gln	Glu	Cys	Leu	Phe	20	25	30
Phe	Asn	Ala	Asn	Trp	Glu	Lys	Asp	Arg	Thr	Asn	Gln	Thr	Gly	Val	Glu	35	40	45
Pro	Cys	Tyr	Gly	Asp	Lys	Asp	Lys	Arg	Arg	His	Cys	Phe	Ala	Thr	Trp	50	55	60
Lys	Asn	Ile	Ser	Gly	Ser	Ile	Glu	Ile	Val	Lys	Gln	Gly	Cys	Trp	Leu	65	70	75
Asp	Asp	Ile	Asn	Cys	Tyr	Asp	Arg	Thr	Asp	Cys	Val	Glu	Lys	Lys	Asp	85	90	95
Ser	Pro	Glu	Val	Tyr	Phe	Cys	Cys	Cys	Glu	Gly	Asn	Met	Cys	Asn	Glu	100	105	110
Lys	Phe	Ser	Tyr	Phe	Pro	Glu	Met	Glu	Val	Thr	Gln	Pro	Thr	Ser	Asn			

```

      115              120              125
Pro Val Thr Pro Lys Pro Pro Tyr Tyr Asn Ile Leu Leu Tyr Ser Leu
  130              135              140
Val Pro Leu Met Leu Ile Ala Gly Ile Val Ile Cys Ala Phe Trp Val
  145              150              155              160
Tyr Arg His His Lys Met Ala Tyr Pro Pro Val Leu Val Pro Thr Gln
      165              170              175
Asp Pro Gly Pro Pro Pro Pro Ser Pro Leu Leu Gly Leu Lys Pro Leu
      180              185              190
Gln Leu Leu Glu Val Lys Ala Arg Gly Arg Phe Gly Cys Val Trp Lys
      195              200              205
Ala Gln Leu Leu Asn Glu Tyr Val Ala Val Lys Ile Phe Pro Ile Gln
      210              215              220
Asp Lys Gln Ser Trp Gln Asn Glu Tyr Glu Val Tyr Ser Leu Pro Gly
  225              230              235              240
Met Lys His Glu Asn Ile Leu Gln Phe Ile Gly Ala Glu Lys Arg Gly
      245              250              255
Thr Ser Val Asp Val Asp Leu Trp Leu Ile Thr Ala Phe His Glu Lys
      260              265              270
Gly Ser Leu Ser Asp Phe Leu Lys Ala Asn Val Val Ser Trp Asn Glu
      275              280              285
Leu Cys His Ile Ala Glu Thr Met Ala Arg Gly Leu Ala Tyr Leu His
      290              295              300
Glu Asp Ile Pro Gly Leu Lys Asp Gly His Lys Pro Ala Ile Ser His
  305              310              315              320
Arg Asp Ile Lys Ser Lys Asn Val Leu Leu Lys Asn Asn Leu Thr Ala
      325              330              335
Cys Ile Ala Asp Phe Gly Leu Ala Leu Lys Phe Glu Ala Gly Lys Ser
      340              345              350
Ala Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro
      355              360              365
Glu Val Leu Glu Gly Ala Ile Asn Phe Gln Arg Asp Ala Phe Leu Arg
      370              375              380
Ile Asp Met Tyr Ala Met Gly Leu Val Leu Trp Glu Leu Ala Ser Arg
  385              390              395              400
Cys Thr Ala Ala Asp Gly Pro Val Asp Glu Tyr Met Leu Pro Phe Glu
      405              410              415
Glu Glu Ile Gly Gln His Pro Ser Leu Glu Asp Met Gln Glu Val Val
      420              425              430
Val His Lys Lys Lys Arg Pro Val Leu Arg Asp Tyr Trp Gln Lys His
      435              440              445
Ala Gly Met Ala Met Leu Cys Glu Thr Ile Glu Glu Cys Trp Asp His
      450              455              460
Asp Ala Glu Ala Arg Leu Ser Ala Gly Cys Val Gly Glu Arg Ile Thr
  465              470              475              480
Gln Met Gln Arg Leu Thr Asn Ile Ile Thr Thr Glu Asp Ile Val Thr
      485              490              495
Val Val Thr Met Val Thr Asn Val Asp Phe Pro Pro Lys Glu Ser Ser
      500              505              510
Leu

```

(2) INFORMATION FOR SEQ ID NO: 31:-

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

```

Met Thr Ala Pro Trp Ala Ala Leu Ala Leu Leu Trp Gly Ser Leu Cys
      5      10      15
Ala Gly Ser Gly Arg Gly Glu Ala Glu Thr Arg Glu Cys Ile Tyr Tyr
      20      25      30
Asn Ala Asn Trp Glu Leu Glu Arg Thr Asn Gln Ser Gly Leu Glu Arg
      35      40      45
Cys Glu Gly Glu Gln Asp Lys Arg Leu His Cys Tyr Ala Ser Trp Arg
      50      55      60
Asn Ser Ser Gly Thr Ile Glu Leu Val Lys Lys Gly Cys Trp Leu Asp
      65      70      75      80
Asp Phe Asn Cys Tyr Asp Arg Gln Glu Cys Val Ala Thr Glu Glu Asn
      85      90      95
Pro Gln Val Tyr Phe Cys Cys Cys Glu Gly Asn Phe Cys Asn Glu Arg
      100      105      110
Phe Thr His Leu Pro Glu Pro Gly Gly Pro Glu Val Thr Tyr Glu Pro
      115      120      125
Pro Pro Thr Ala Pro Thr Leu Leu Thr Val Leu Ala Tyr Ser Leu Leu
      130      135      140
Pro Ile Gly Gly Leu Ser Leu Ile Val Leu Leu Ala Phe Trp Met Tyr
      145      150      155      160
Arg His Arg Lys Pro Pro Tyr Gly His Val Asp Ile His Glu Val Arg
      165      170      175
Gln Cys Gln Arg Trp Ala Gly Arg Arg Asp Gly Cys Ala Asp Ser Phe
      180      185      190
Lys Pro Leu Pro Phe Gln Asp Pro Gly Pro Pro Pro Pro Ser Pro Leu
      195      200      205
Val Gly Leu Lys Pro Leu Gln Leu Leu Glu Ile Lys Ala Arg Gly Arg
      210      215      220
Phe Gly Cys Val Trp Lys Ala Gln Leu Met Asn Asp Phe Val Ala Val
      225      230      235      240
Lys Ile Phe Pro Leu Gln Asp Lys Gln Ser Trp Gln Ser Glu Arg Glu
      245      250      255
Ile Phe Ser Thr Pro Gly Met Lys His Glu Asn Leu Leu Gln Phe Ile
      260      265      270
Ala Ala Glu Lys Arg Gly Ser Asn Leu Glu Val Glu Leu Trp Leu Ile
      275      280      285
Thr Ala Phe His Asp Lys Gly Ser Leu Thr Asp Tyr Leu Lys Gly Asn
      290      295      300
Ile Ile Thr Trp Asn Glu Leu Cys His Val Ala Glu Thr Met Ser Arg
      305      310      315      320
Gly Leu Ser Tyr Leu His Glu Asp Val Pro Trp Cys Arg Gly Glu Gly
      325      330      335
His Lys Pro Ser Ile Ala His Arg Asp Phe Lys Ser Lys Asn Val Leu
      340      345      350
Leu Lys Ser Asp Leu Thr Ala Val Leu Ala Asp Phe Gly Leu Ala Val
      355      360      365
Arg Phe Glu Pro Gly Lys Pro Pro Gly Asp Thr His Gly Gln Val Gly
      370      375      380
Thr Arg Arg Tyr Met Ala Pro Glu Val Leu Glu Gly Ala Ile Asn Phe
      385      390      395      400
Gln Arg Asp Ala Phe Leu Arg Ile Asp Met Tyr Ala Met Gly Leu Val
      405      410      415
Leu Trp Glu Leu Val Ser Arg Cys Lys Ala Ala Asp Gly Pro Val Asp
      420      425      430
Glu Tyr Met Leu Pro Phe Glu Glu Glu Ile Gly Gln His Pro Ser Leu

```

```

      435              440              445
Glu Glu Leu Gln Glu Val Val Val His Lys Lys Met Arg Pro Thr Ile
  450              455              460
Lys Asp His Trp Leu Lys His Pro Gly Leu Ala Gln Leu Cys Val Thr
  465              470              475              480
Ile Glu Glu Cys Trp Asp His Asp Ala Glu Ala Arg Leu Ser Ala Gly
      485              490              495
Cys Val Glu Glu Arg Val Ser Leu Ile Arg Arg Ser Val Asn Gly Thr
      500              505              510
Thr Ser Asp Cys Leu Val Ser Leu Val Thr Ser Val Thr Asn Val Asp
      515              520              525
Leu Leu Pro Lys Glu Ser Ser Ile
      530              535

```

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 567 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

```

Met Gly Arg Gly Leu Leu Arg Gly Leu Trp Pro Leu His Ile Val Leu
      5              10              15
Trp Thr Arg Ile Ala Ser Thr Ile Pro Pro His Val Gln Lys Ser Val
      20              25              30
Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro
      35              40              45
Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln
      50              55              60
Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro
      65              70              75              80
Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr
      85              90              95
Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile
      100              105              110
Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys
      115              120              125
Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn
      130              135              140
Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Leu
      145              150              155              160
Leu Leu Val Ile Phe Gln Val Thr Gly Ile Ser Leu Leu Pro Pro Leu
      165              170              175
Gly Val Ala Ile Ser Val Ile Ile Ile Phe Tyr Cys Tyr Arg Val Asn
      180              185              190
Arg Gln Gln Lys Leu Ser Ser Thr Trp Glu Thr Gly Lys Thr Arg Lys
      195              200              205
Leu Met Glu Phe Ser Glu His Cys Ala Ile Ile Leu Glu Asp Asp Arg
      210              215              220
Ser Asp Ile Ser Ser Thr Cys Ala Asn Asn Ile Asn His Asn Thr Glu
      225              230              235              240
Leu Leu Pro Ile Glu Leu Asp Thr Leu Val Gly Lys Gly Arg Phe Ala
      245              250              255
Glu Val Tyr Lys Ala Lys Leu Lys Gln Asn Thr Ser Glu Gln Phe Glu
      260              265              270
Thr Val Ala Val Lys Ile Phe Pro Tyr Glu Glu Tyr Ala Ser Trp Lys

```

```

      275              280              285
Thr Glu Lys Asp Ile Phe Ser Asp Ile Asn Leu Lys His Glu Asn Ile
 290              295              300
Leu Gln Phe Leu Thr Ala Glu Glu Arg Lys Thr Glu Leu Gly Lys Gln
 305              310              315              320
Tyr Trp Leu Ile Thr Ala Phe His Ala Lys Gly Asn Leu Gln Glu Tyr
      325              330              335
Leu Thr Arg His Val Ile Ser Trp Glu Asp Leu Arg Lys Leu Gly Ser
      340              345              350
Ser Leu Ala Arg Gly Ile Ala His Leu His Ser Asp His Thr Pro Cys
      355              360              365
Gly Arg Pro Lys Met Pro Ile Val His Arg Asp Leu Lys Ser Ser Asn
 370              375              380
Ile Leu Val Lys Asn Asp Leu Thr Cys Cys Leu Cys Asp Phe Gly Leu
 385              390              395              400
Ser Leu Arg Leu Asp Pro Thr Leu Ser Val Asp Asp Leu Ala Asn Ser
      405              410              415
Gly Gln Val Gly Thr Ala Arg Tyr Met Ala Pro Glu Val Leu Glu Ser
      420              425              430
Arg Met Asn Leu Glu Asn Ala Glu Ser Phe Lys Gln Thr Asp Val Tyr
      435              440              445
Ser Met Ala Leu Val Leu Trp Glu Met Thr Ser Arg Cys Asn Ala Val
 450              455              460
Gly Glu Val Lys Asp Tyr Glu Pro Pro Phe Gly Ser Lys Val Arg Glu
 465              470              475              480
His Pro Cys Val Glu Ser Met Lys Asp Asn Val Leu Arg Asp Arg Gly
      485              490              495
Arg Pro Glu Ile Pro Ser Phe Trp Leu Asn His Gln Gly Ile Gln Met
      500              505              510
Val Cys Glu Thr Leu Thr Glu Cys Trp Asp His Asp Pro Glu Ala Arg
      515              520              525
Leu Thr Ala Gln Cys Val Ala Glu Arg Phe Ser Glu Leu Glu His Leu
 530              535              540
Asp Arg Leu Ser Gly Arg Ser Cys Ser Glu Glu Lys Ile Pro Glu Asp
 545              550              555              560
Gly Ser Leu Asn Thr Thr Lys
      565

```

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

```

Leu Thr Gly Arg Val Gly Ser Gly Arg Phe Gly Asn Val Ser Arg Gly
   5              10              15
Asp Tyr Arg Gly Glu Ala Val Ala Val Lys Val Phe Asn Ala Ile Asp
  20              25              30
Glu Pro Ala Phe His Lys Glu Ile Glu Ile Phe Glu Thr Arg Met Leu
  35              40              45
Arg His Pro Asn Val Leu Arg Tyr Ile Gly Ser Asp Arg Val Asp Thr
  50              55              60
Gly Phe Val Thr Glu Leu Trp Leu Val Ile Glu Tyr His Pro Ser Gly
  65              70              75              80
Ser Leu His Asp Phe Leu Leu Glu Asn Thr Val Asn Ile Glu Thr Tyr

```



```

      85              90              95
Tyr Asn Leu Met Arg Ser Thr Ala Ser Gly Leu Ala Phe Leu His Asn
      100              105              110
Gln Ile Gly Gly Ser Lys Glu Ser Asn Lys Pro Ala Met Ala His Arg
      115              120              125
Asp Ile Lys Ser Lys Asn Ile Met Tyr Lys Asn Asp Leu Thr Cys Ala
      130              135              140
Ile Gly Asp Leu Gly Leu Ser Leu Ser Lys Pro Glu Asp Ala Ala Ser
      145              150              155              160
Asp Ile Ile Ala Asn Glu Asn Tyr Lys Cys Gly Thr Val Arg Tyr Leu
      165              170              175
Ala Pro

```

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34

```

Thr Arg Leu His Leu Cys His Cys Ser Arg Glu Val Gly Cys Asn Ala
      5              10              15
Arg Thr Thr Gly Trp Val Pro Gly Ile Glu Phe Leu Asn Glu Thr Asp
      20              25              30
Arg Ser Phe Tyr Glu Asn Thr Cys Tyr Thr Asp Gly Ser Cys Tyr Gln
      35              40              45
Ser Ala Arg Pro Ser Pro Glu Ile Ser His Phe Gly Cys Met Asp Glu
      50              55              60
Lys Ser Val Thr Asp Glu Thr Glu Phe His Asp Thr Ala Ala Lys Val
      65              70              75              80
Cys Thr Asn Asn Thr Lys Asp Pro His Ala Thr Val Trp Ile Cys Cys
      85              90              95
Asp Lys Gly Asn Phe Cys Ala Asn Glu Thr Ile Ile His Leu Ala Pro
      100              105              110
Gly Pro Gln Gln Ser Ser Thr Trp Leu Ile Leu Thr Ile Leu Ala Leu
      115              120              125
Leu Thr
      130

```

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

```

Asp Leu Lys Pro Glu Asn
      5

```

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(v) FRAGMENT TYPE: internal
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:
Asp Leu Ala Ala Arg Asn
5

(2) INFORMATION FOR SEQ ID NO: 37:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(v) FRAGMENT TYPE: internal
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:
Gly Thr Xaa Xaa Tyr Xaa
5

(2) INFORMATION FOR SEQ ID NO: 38:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(v) FRAGMENT TYPE: internal
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:
Gly Thr Xaa Xaa Phe Xaa
5

(2) INFORMATION FOR SEQ ID NO: 39:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(v) FRAGMENT TYPE: internal
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:
Gly Ser Xaa Xaa Tyr Xaa
5

(2) INFORMATION FOR SEQ ID NO: 40:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(v) FRAGMENT TYPE: internal
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:
Gly Ser Xaa Xaa Phe Xaa
5

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(v) FRAGMENT TYPE: internal
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:
Xaa Pro Ile Lys Trp Thr
 5

(2) INFORMATION FOR SEQ ID NO: 42:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (v) FRAGMENT TYPE: internal
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:
Xaa Pro Ile Lys Trp Met
 5

(2) INFORMATION FOR SEQ ID NO: 43:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (v) FRAGMENT TYPE: internal
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:
Xaa Pro Ile Arg Trp Thr
 5

(2) INFORMATION FOR SEQ ID NO: 44:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (v) FRAGMENT TYPE: internal
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:
Xaa Pro Ile Arg Trp Met
 5

(2) INFORMATION FOR SEQ ID NO: 45:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (v) FRAGMENT TYPE: internal
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:
Xaa Pro Val Lys Trp Thr
 5

(2) INFORMATION FOR SEQ ID NO: 46:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (v) FRAGMENT TYPE: internal
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:
Xaa Pro Val Lys Trp Met
 5

(2) INFORMATION FOR SEQ ID NO: 47:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (v) FRAGMENT TYPE: internal
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:
Xaa Pro Val Arg Trp Thr
 5

(2) INFORMATION FOR SEQ ID NO: 48:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (v) FRAGMENT TYPE: internal
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:
Xaa Pro Val Arg Trp Met
 5